

## Microbial Properties Database Editor Tutorial

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## Summary

A Microbial Properties Database Editor (MPDBE) has been developed to help consolidate microbial-relevant data to populate a microbial database and support a database editor by which an authorized user can modify physico-microbial properties related to microbial indicators and pathogens. Physical properties describe changes in state of the physical system and relate to properties such as mass of a microbe, excretion density of microbes in animal feces, prevalence, etc. Microbial properties relate to changes in or with the microbe, such as inactivation rate, attachment/detachment rates, dose-response coefficients, etc. The objective of the MPDBE is to provide a tool by which an authorized user can modify physico-microbial properties related to microbial indicators and pathogens and populate metadata standards, so the properties are available for consumption by microbial source, fate, transport, and risk models. Although other databases are being developed on specific microbial properties, such as inactivation of microorganisms in environmental media, or explicitly include other valuable support information (e.g., methods of analysis, experimental set up, etc.), this database helps bridge the gap between modeling, monitoring, and methods by identifying parameters that are typically used by models engaged in Quantitative Microbial Risk Assessments (QMRAs). These parameters address modeling paradigms that include release mechanism from manure forms (e.g., solid pats, slurry, and dry litter); fate and transport through various environmental media (e.g., overland, groundwater, surface water); exposure; intake; and risk. Some parameters may be widely used (e.g., inactivation rates), while others may seem obscure but only because users may not be familiar with the specific models or the literature associated with them. As additional parameters are correlated to more models, these can be added to the database to ensure a smooth linkage between data collected in the field and at the bench-scale with models that consume the information. Once populated, the database can act as a reference to help parameterize models used in QMRAs. In addition, for models registered to integrated environmental modeling infrastructures, the database editor could be used to automatically populate model input requirements. The microbial database is to supply microbial properties to users. Included with the microbial database will be an editor that lets users update microbial and parameter values in the database. The parameters for evaluation of impacts due to pathogen exposure can be viewed, estimated, modified, printed, deleted, and exported.

# Microbial Properties Database Editor Tutorial

## PURPOSE

To help consolidate microbial-relevant data to populate a microbial database and support a database editor by which an authorized user can modify physico-microbial properties related to microbial indicators and pathogens. Physical properties describe the changes in state of the physical system and relate to properties such as mass of a microbe, excretion density of microbes in animal feces, prevalence, etc. Microbial properties relate to changes in or with the microbe, such as inactivation rate, attachment/detachment rates, dose-response coefficients, etc.

## OBJECTIVE

To develop a database editor by which an authorized user can modify physico-microbial properties related to microbial indicators and pathogens and to populate metadata standards, so the properties are available for consumption by microbial source, fate, transport, and risk modules; the intent is to make available microbial properties for multimedia modeling components. The Microbial Properties Database Editor may be used to access, edit, update, modify, or correct 1) the permanent database, and 2) a temporary database to be made available for modeling components used within an integrated environmental modeling workflow.

## BACKGROUND

Whelan et al. (2014a) note that a Quantitative Microbial Risk Assessment (QMRA) characterizes potential human health risk using four pieces of information: average pathogen densities, mean water ingestion for the exposure scenario, pathogen dose-response relationships, and conditional probability of illness (Haas et al., 1999; Hunter et al., 2003). The risk assessment approach differs from epidemiological approaches (Calderon et al., 1991; Colford et al., 2012; Haile et al., 1999) in that the latter seek to associate levels of self-reported disease (e.g., in a group of swimmers) with the water quality measured by fecal indicator bacteria, and not the etiological agent(s) responsible for the disease. Epidemiology studies implicitly characterize the source of fecal contamination, fate and transport kinetics of the microbes, the natural variability of the microbes in the environmental matrix, the etiological agent(s) and exposure scenario studied, while QMRA deals explicitly with these components. Although researchers can survey the literature and extract information relevant to their QMRA modeling activities, these unrelated surveys can result in different, inconsistent, and contradictory QMRA assessments, as a consistent mapping between modeling, monitoring, and methods has not been institutionalized.

Although other databases are being developed on specific microbial properties, such as inactivation of microorganisms in environmental media (Pachepsky et al., 2010), or explicitly include other valuable support information (e.g., methods of analysis, experimental set up, etc.), this database helps bridge the gap between modeling, monitoring, and methods by identifying parameters that are typically used by models engaged in QMRA assessments. These parameters address modeling paradigms that include release mechanism from manure forms (e.g., solid pats, slurry, and dry litter); fate and transport through various environmental media (e.g., overland, groundwater, surface water); exposure; intake;

and risk. Some parameters may be widely used (e.g., inactivation rates), while others may seem obscure but only because users may not be familiar with the specific models or the literature associated with them. Although there is no common classification of manures, typically one distinguishes liquid manure or slurry (less solid fraction), sludge (e.g., lagoon material), dry litter, and pastureland animal waste (e.g., cowpats), although sometimes farmyard manure (more solid fraction) is designated. For simplification, these categories have been combined into three designations: Solid, Slurry, and Dry Litter. As additional parameters are used in more models, these can be added to the database to ensure a smooth linkage between data collected in the field and at the bench-scale with models that consume the information. Once populated, the database can act as a reference help parameterize models used in QMRAs. In addition, for models registered to integrated environmental modeling infrastructures (Whelan et al., 2014b; Laniak et al., 2013), the database editor can be used to automatically populate model input requirements, as illustrated by Whelan et al. (2014a).

## PARAMETERS CONTAINED IN THE MICROBIAL PROPERTIES DATABASE

Table 1 lists the parameters contained in the Microbial Properties Database with definitions. The list has been compiled using input needs of models that can be, and traditionally have been, used in microbial assessments investigating microbial release mechanisms from manure (Bradford and Schijven, 2002; Kim et al., 2015; Guber et al., 2010, 2013) and supporting fate and transport modeling, watershed modeling (Bicknell et al., 1997; EPA 2013b, 2013c), and exposure and risk assessment modeling (Soller et al., 2008, 2004). Table 2 expands on Table 1's first seven parameters (Name, LandUseName, DomesticAnimalName, WildLifeName, UrbanizedName, MediumName, and ManureForm), since they describe indices associated with other microbial parameters in Table 1. Table 3 combines Tables 1 and 2 to create the Microbial Properties Database ontological dictionary which groups similar and related parameters and provides a single naming convention for variables and parameters shared by modeling components (Whelan et al., 2014b). Table 3 provides the following specific information:

- Variable Name
- Variable Description/Definition
- Variable Dimension/Cardinality – Number of elements in a set or other grouping, as a property of that variable. For example, if the variable “concentration” is a function of chemical name, location, and time, then it would have a dimension of 3.
- Variable Data Type – String, Float, Integer, Logical
- Primary Key – Variables that can only be identified and defined once in a workflow ontology (i.e., universal parameter recognized by all components within a workflow).
- Scaler – Indicates that the variable is not part of a list. If it is part of a list, then it is considered self-indexed (a function of itself) or self-enumerated (specified one after another). For example, a time series is typically self-indexed, so the first time is indexed to 1, the second time is indexed to 2, etc. Self-indexing (i.e., being non-scaler) increases the Variable Dimension by one.
- Variable Range – Minimum and Maximum
- Measure — Categorizes a collection of units that inherit the same measuring properties; for example, meter, foot, and yard are units for the measure “Length.”
- Variable's Units – Scaling properties within the same measure.
- Stochastic – Identifies variables available for statistical manipulation, such as Monte Carlo
- Indices – Elements in a set or other grouping, as a property of that variable (other parameters of which this variable is a function; see Table 2).

**Table 1.** Parameter names and descriptions in the Microbial Properties Database

Parameter Name	Parameter Description
Name	Name of microbe
LandUseName	Land Use Type
DomesticAnimalName	Domestic Animal Name
WildLifeName	Wildlife Name
UrbanizedName	Name of Mixed Urban or Built up area
MediumName	Environmental Medium associated with Microbe
ManureForm	Physical form of the manure (solid, slurry, dry litter)
AlphaM	Fitting parameter that controls the initial microbial release rate from the manure (Bradford and Schijven, 2002)
Bman	The fitting parameter defining the shape of the Microbe manure-release curve (Bman) (Bradford and Schijven, 2002)
ReleaseRateEff	Microbial release rate efficiency from the manure (which is constant with time); it is the fraction of the microbes that are actually released from the manure (Er) (Bradford and Schijven, 2002)
ReleaseRateEffConstant	A Constant parameter that reflects the microbial release rate efficiency from the manure; the release rate efficiency varies with time (b) (Kim et al., 2015)
ExcretionDensity	Density of microbe in feces of animal per wet weight
ExcretionDensitySuperShedder	Density of microbe in feces of animal that is a super shedder per wet weight
FastDieOffManure	Fast stage microbial inactivation rate by manure form (Blaustein et al., 2013)
PartitionCoef	Instantaneous partition coefficient between liquid and solid phases (traditional distribution coefficient, Kd)
Prevalence	Fraction of the animals infected with pathogen
SlowDieOffManure	Slow stage microbial inactivation rate by manure form (Blaustein et al., 2013)
BetaPoissonConst	Constant shape parameter in Beta Poisson Dose-Response Model (Haas et al., 1999)
BetaPoissonExp	Exponent shape parameter in Beta Poisson Dose-Response Model (Haas et al., 1999)
ExpoDoseRespConst	Constant parameter (r) in Exponential Dose-Response model (Haas et al., 1999)
GompertzLogFirstConst	First parameter (a) in Gompertz-log Dose-Response model (Haas et al., 1999)
GompertzLogSecondConst	Second parameter (b) in Gompertz-log Dose-Response model (Haas et al., 1999)
HypergeometricFirstConst	First parameter (a) in Hypergeometric Dose-Response model (Haas et al., 1999)
HypergeometricSecondConst	Second parameter (b) in Hypergeometric Dose-Response model (Haas et al., 1999)
AttachRate	Attachment rate of Microbe at the soil-solid phase (ka in KINEROS2/STWIR) (Guber et al., 2010)

DetachRate	Detachment rate of Microbe at the soil-solid phase (lower case kd in KINEROS2/STWIR) (Guber et al., 2010)
ExchangeDepth	Thickness of top layer that actively interacts with overland flow (i.e., mixing zone) (Guber et al., 2010)
InfilFracKf	Fraction of infiltrated cells that have been filtered out by the soil mixing zone (i.e., staying in mixing zone) (kf in Model 2 KINEROS2/STWIR) (Guber et al., 2010)
MassTransferRateK	Mass Transfer Rate of Microbe at the soil-solid phase interface (k in Model 1 KINEROS2/STWIR) (Guber et al., 2010)
StrainCoef	Straining coefficient, referring to losses due to infiltration (unity is not infiltration loss) (kstr in KINEROS2/STWIR) (Guber et al., 2010)
SepticConc	Typical microbial concentration in septic system waste
Infect_asymtomatic	Duration of asymptomatic infection in days
Infect_endemic	Beta_end (endemic transmission rate) (Soller et al., 2008, 2004)
Infect_incubation	Duration of incubation in days (Soller et al., 2008, 2004)
Infect_p_to_p	Beta_pp (person-person transmission rate) (Soller et al., 2008, 2004)
Infect_reinfect	Duration of protection from reinfection in days (Soller et al., 2008, 2004)
Infect_response	Probability of symptomatic response, expressed as a fraction (Soller et al., 2008, 2004)
Infect_symtomatic	Duration of symptomatic infection in days (Soller et al., 2008, 2004)
AnimalConcMass	Microbial concentration based on mass of waste shed by domestic animal
AnimalShedRateMass	Domestic animal shedding rate in mass of waste (weight weight) per time
BuiltUpRate	Accumulation rates in median microbial counts per area per time by built up (i.e., urbanized) land use
DieOffManure	First-order microbial inactivation/die-off rate by manure form
DieOffMedium	First-order microbial inactivation/die-off rate by environmental medium
DieOffTempCorr	Microbial inactivation/Die-off rate Temperature Correction
Mass	Mass of a single microbe
WildLifeDensity	Typical number of wildlife per unit area by landuse pattern
WildLifeShedRate	Typical wildlife microbial shedding rate per wildlife

**Table 2.** Indices associated with Parameters

Index	Definition
Name	<p>Microbe Name. There are 17 microbes currently registered by microbe type (Indicator or Pathogen) and class (Bacterial, Protozoa, or Virus):</p> <ul style="list-style-type: none"> <li>• Indicator Bacteria               <ol style="list-style-type: none"> <li>1. E. coli</li> <li>2. Enterococci</li> <li>3. Clostridium perfringens</li> <li>4. Fecal Coliforms</li> <li>5. Bacteroides</li> </ol> </li> <li>• Pathogenic Bacteria               <ol style="list-style-type: none"> <li>6. Salmonella spp</li> <li>7. Campylobacter spp</li> <li>8. E. coli O157:H7</li> <li>9. Listeria</li> <li>10. Mycobacterium avium paratuberculosis</li> </ol> </li> <li>• Pathogenic Protozoa               <ol style="list-style-type: none"> <li>11. Cryptosporidium parvum</li> <li>12. Giardia lamblia</li> <li>13. Toxoplasma gondii</li> </ol> </li> <li>• Pathogenic Viruses               <ol style="list-style-type: none"> <li>14. Enterovirus</li> <li>15. Rotavirus</li> <li>16. Adenovirus</li> <li>17. Norovirus</li> </ol> </li> </ul>
DomesticAnimalName	<p>Domestic Animal Name. There are seven domestic animal name designations:</p> <ol style="list-style-type: none"> <li>1. DairyCow: Dairy Cow</li> <li>2. BeefCow: Beef Cattle</li> <li>3. Swine</li> <li>4. Poultry</li> <li>5. Horse</li> <li>6. Sheep</li> <li>7. OtherAgAnimal: Other Agricultural Animal</li> </ol>
LandUseName	<p>Landuse Type. There are four landuse type designations:</p> <ol style="list-style-type: none"> <li>1. Forest</li> <li>2. Cropland</li> <li>3. Pasture</li> <li>4. Urbanized (a.k.a. Builtup)</li> </ol>
UrbanizedName	<p>Name of Urbanized or Builtup areas. There are four Urbanized designations:</p> <ol style="list-style-type: none"> <li>1. CommercialAndServices: Commercial and Services</li> <li>2. Residential</li> <li>3. MixedUrban: MixedUrban</li> <li>4. TransportationCommunicationUtilities: Transportation, Communication, Utilities</li> </ol>
WildlifeName	<p>Wildlife Name: There are six wildlife name designations:</p> <ol style="list-style-type: none"> <li>1. Duck</li> </ol>

	<ol style="list-style-type: none"> <li>2. Goose</li> <li>3. Deer</li> <li>4. Beaver</li> <li>5. Raccoon</li> <li>6. OtherWildlife: Other Wildlife</li> </ol>
ManureForm	<p>Physical form of the manure. There are three designations:</p> <ol style="list-style-type: none"> <li>1. Solid</li> <li>2. Slurry</li> <li>3. Dry Litter</li> </ol>
MediumName	<p>Name of environmental medium associated with Microbe. There are 11 medium designations:</p> <ol style="list-style-type: none"> <li>1. Air</li> <li>2. VadoseZone</li> <li>3. Aquifer</li> <li>4. Impoundment (e.g., pond, reservoir)</li> <li>5. WasteStoragePond</li> <li>6. SurfaceWater (e.g., river, stream)</li> <li>7. Soil</li> <li>8. Sediments</li> <li>9. Stormwater</li> <li>10. WastewaterEffluent</li> <li>11. GrayWater</li> </ol>

**Table 3. Microbial Properties Database Ontological Dictionary**

NAME	Parameter Description	Dimension	Data Type	Primary Key	Not Self-indexed?	Minimum	Maximum	Measure	Units	Stochastic?	Index 1	Index 2	Index 3
Name	Name of microbe	1	STRING	FALSE	FALSE					FALSE			
LandUseName	Land Use Type	1	STRING	FALSE	FALSE					FALSE			
DomesticAnimalName	Domestic Animal Name	1	STRING	FALSE	FALSE					FALSE			
WildLifeName	Wildlife Name	1	STRING	FALSE	FALSE					FALSE			
UrbanizedName	Name of Mixed Urban or Built up area	1	STRING	FALSE	FALSE					FALSE			
MediumName	Environmental Medium associated with Microbe	1	STRING	FALSE	FALSE					FALSE			
ManureForm	Physical form of the manure (solid, slurry, dry litter)	1	STRING	FALSE	FALSE					FALSE			
WildLifeDensity	Typical number of wildlife per unit area by landuse pattern	2	FLOAT	FALSE	TRUE	0	1.0E+38	Unitless/Area	Number/ac	TRUE	LandUseName	WildLifeName	
WildLifeShedRate	Typical wildlife microbial shedding rate per wildlife	2	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts/Time	Microbial Counts/d	TRUE	Name	WildLifeName	
AnimalShedRateMass	Domestic animal shedding rate in mass of waste (ww) per time	1	FLOAT	FALSE	TRUE	0	1.0E+38	Mass/Time	Kg/d	TRUE	DomesticAnimalName		
AnimalConcMass	Microbial concentration based on mass of waste shed by domestic animal	2	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts/Mass	Microbial Counts/g	TRUE	Name	DomesticAnimalName	
SepticConc	Typical microbial concentration in septic system waste	1	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts/Volume	Microbial Counts/L	TRUE	Name		
BuiltUpRate	Accumulation rates in median microbial counts per area per time by built up land use	3	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts/Area/Time	Microbial Counts/ac/d	TRUE	Name	LandUseName	UrbanizedName
Mass	Mass of a single microbe	1	FLOAT	FALSE	TRUE	0	1.0E+38	Mass	g	TRUE	Name		
DieOffMedium	First-order microbial inactivation/die-off rate by medium	2	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/d	TRUE	Name	MediumName	
DieOffManure	First-order microbial inactivation/die-off rate by manure form	3	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/d	TRUE	Name	DomesticAnimalName	ManureForm
DieOffTempCorr	Microbial inactivation/Die-off rate Temperature Correction	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
SlowDieOffManure	Slow phase (dark) microbial inactivation rate by manure form	3	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/d	TRUE	Name	DomesticAnimalName	ManureForm
FastDieOffManure	Fast phase (light) microbial inactivation rate by manure form	3	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/d	TRUE	Name	DomesticAnimalName	ManureForm
Prevalence	Fraction of the animals infected with microbe	2	FLOAT	FALSE	TRUE	0	1.0	Ratio	Fraction	TRUE	Name	DomesticAnimalName	
ExcretionDensity	Density of microbe in feces of infected animal per ww	2	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts/Mass	Microbial Counts/g	TRUE	Name	DomesticAnimalName	
ExcretionDensitySuperShedder	Density of microbe in feces of infected animal that is a super shedder per ww	2	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts/Mass	Microbial Counts/g	TRUE	Name	DomesticAnimalName	
PartitionCoef	Instantaneous partition coefficient between liquid and solid phases (traditional distribution coefficient, Kd)	2	FLOAT	FALSE	TRUE	0	1.0E+38	Volume/Mass	mL/g	TRUE	Name	MediumName	
ExpoDoseRespConst	Constant parameter (r) in Exponential Dose-Response model	1	FLOAT	FALSE	TRUE	0	1.0E+38	1/Microbial Counts	1/Microbial Counts	TRUE	Name		

**Table 3. Microbial Properties Database Ontological Dictionary (cont'd)**

NAME	Parameter Description	Dimension	Data Type	Primary Key	Not Self-indexed?	Minimum	Maximum	Measure	Units	Stochastic?	Index 1	Index 2	Index 3
BetaPoissonExp	Exponent shape parameter in Beta Poisson Dose-Response Model	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
BetaPoissonConst	Constant shape parameter in Beta Poisson Dose-Response Model	1	FLOAT	FALSE	TRUE	0	1.0E+38	Microbial Counts	Microbial Counts	TRUE	Name		
HypergeometricFirstConst	First parameter (a) in Hypergeometric Dose-Response model	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
HypergeometricSecondConst	Second parameter (b) in Hypergeometric Dose-Response model	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
GompertzLogFirstConst	First parameter (a) in Gompertz-log Dose-Response model	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
GompertzLogSecondConst	Second parameter (b) in Gompertz-log Dose-Response model	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
Infect_asymptomatic	Duration of asymptomatic infection in days	1	FLOAT	FALSE	TRUE	0	1.0E+38	Time	days	TRUE	Name		
Infect_endemic	Beta_end (endemic transmission rate)	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
Infect_incubation	Duration of incubation in days	1	FLOAT	FALSE	TRUE	0	1.0E+38	Time	days	TRUE	Name		
Infect_p_to_p	Beta_pp (person-person transmission rate)	1	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	Name		
Infect_reinfect	Duration of protection from reinfection in days	1	FLOAT	FALSE	TRUE	0	1.0E+38	Time	days	TRUE	Name		
Infect_response	Probability of symptomatic response, expressed as a fraction	1	FLOAT	FALSE	TRUE	0	1	Ratio	fraction	TRUE	Name		
Infect_syntomatic	Duration of symptomatic infection in days	1	FLOAT	FALSE	TRUE	0	1.0E+38	Time	days	TRUE	Name		
AttachRate	Attachment rate of Microbe at the soil-solid phase (ka in KINEROS2/STWIR)	3	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/hr	TRUE	Name	MediumName	ManureForm
DetachRate	Detachment rate of Microbe at the soil-solid phase (lower case kd in KINEROS2/STWIR)	3	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/hr	TRUE	Name	MediumName	ManureForm
MassTransferRateK	Mass Transfer Rate of Microbe at the soil-solid phase interface (k in Model 1 KINEROS2/STWIR)	3	FLOAT	FALSE	TRUE	0	1.0E+38	Length/Time	cm/hr	TRUE	Name	MediumName	ManureForm
InfilFracKf	Fraction of infiltrated cells that have been filtered out by the soil mixing zone (i.e., staying in mixing zone) (kf in Model 2 KINEROS2/STWIR)	2	FLOAT	FALSE	TRUE	0	1	Ratio	fraction	TRUE	Name	ManureForm	
StrainCoef	Straining coefficient (kstr in KINEROS2/STWIR)	2	FLOAT	FALSE	TRUE	0	1	Ratio	fraction	TRUE	Name	ManureForm	
ExchangeDepth	Thickness of top layer that actively interacts with overland flow (i.e., mixing zone)	1	FLOAT	FALSE	TRUE	0	1.0E+38	Length	m	TRUE	ManureForm		
AlphaM	Fitting parameter that Controls the initial Microbial release rate from the manure	2	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/hr	TRUE	ManureForm		
Bman	The fitting parameter defining the shape of the Microbe manure-release curve (Bman)	2	FLOAT	FALSE	TRUE	0	1.0E+38			TRUE	ManureForm		
ReleaseRateEffConstant	A Constant parameter that reflects the microbial release rate efficiency from the manure; the release rate efficiency varies with time (b)	2	FLOAT	FALSE	TRUE	0	1.0E+38	1/Time	1/hr	TRUE	Name	ManureForm	
ReleaseRateEff	Microbial release rate efficiency from the manure (which is constant with time); it is the fraction of the microbes that are actually released from the manure (Er)	2	FLOAT	FALSE	TRUE	0	1.0E+38	Ratio	fraction	TRUE	Name	ManureForm	

## DEMONSTRATION

This tutorial reviews some of the screens, icons, and basic functions of downloading the tool and using the Microbial Properties Database Editor (MPDBE):

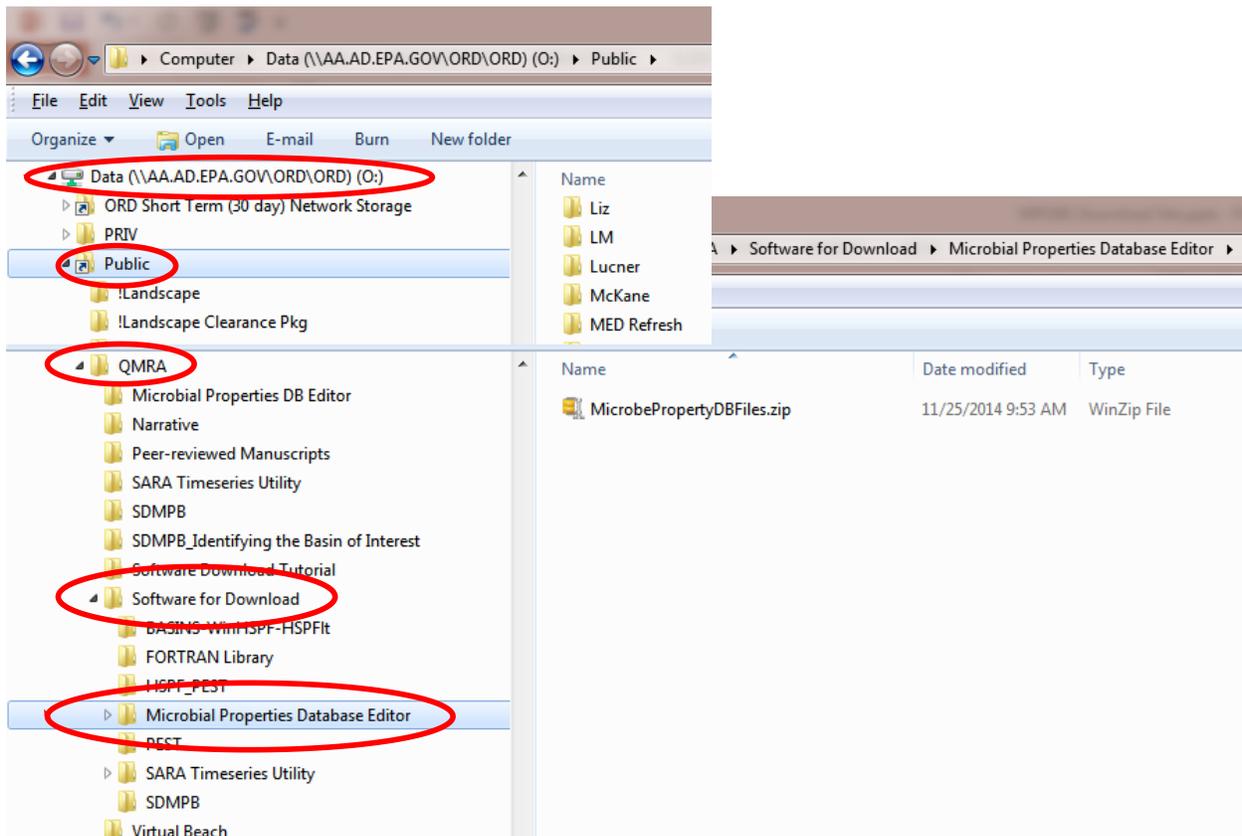
- Software access, retrieval, and download.
- Sort, identify, and select a list of microbes in the database by microbe name, type (i.e., indicator or pathogen) and/or class (i.e., bacteria, protozoa, or virus).
- Edit identification characteristics of existing microbes, or create identification characteristics of a new microbe.
- Edit microbial properties.

## SOFTWARE ACCESS, RETRIEVAL, AND DOWNLOAD

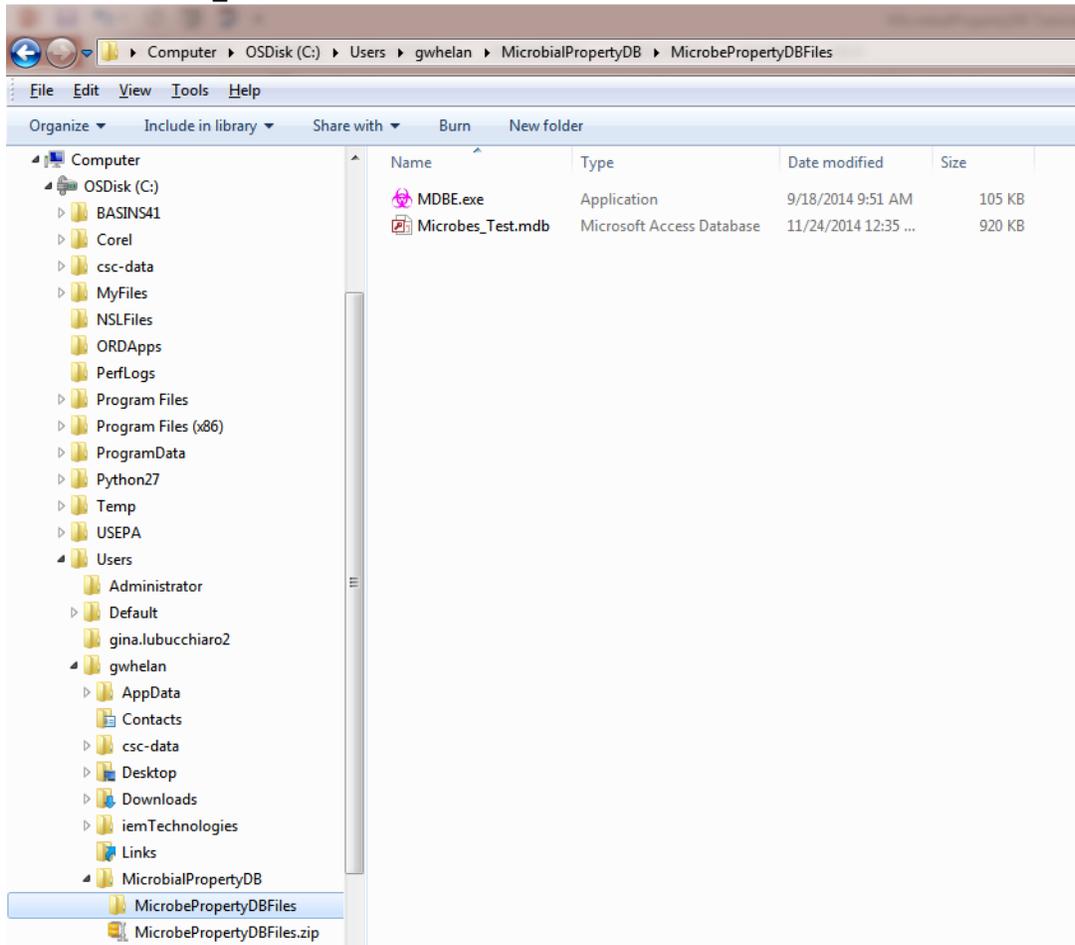
This section describes how to access, retrieve and download the Microbial Properties Database Editor.

1. The Microbial Properties Database Editor software, which is contained in the zip file, titled “MicrobePropertyDBFiles.zip”, can be retrieved from the following site:

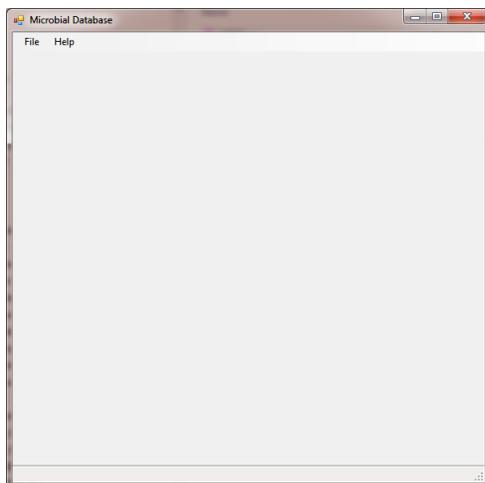
<O:\Public\QMRA\Microbial Properties DB Editor>



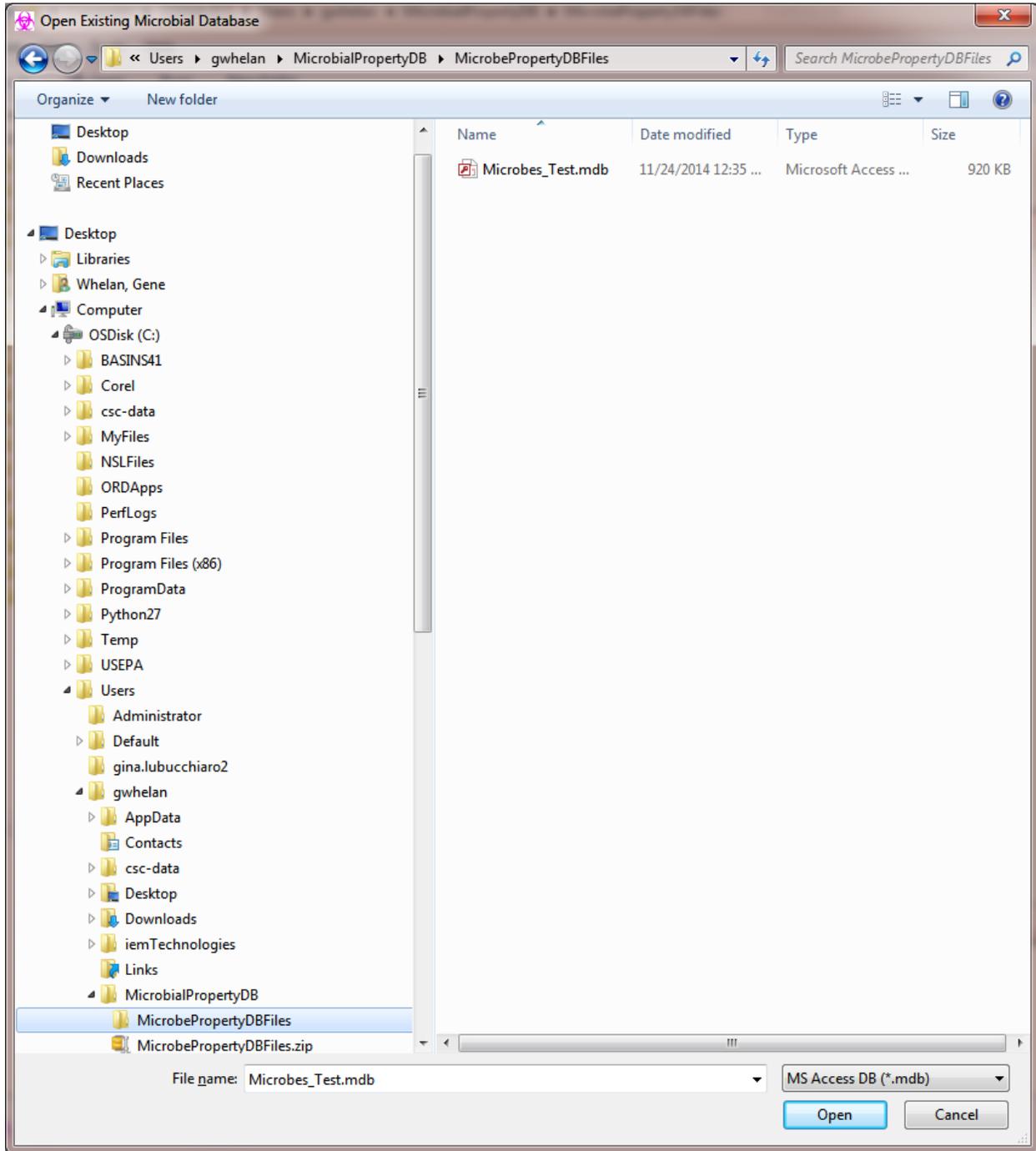
- Unzip or extract the files, creating a folder; in the case below, a folder with the same name (MicrobePropertyDBFiles) was created in the same directory as the zip file. Two files are unzipped or extracted to the MicrobePropertyDBFiles folder: MDBE.exe and Microbes\_Test.mdb.



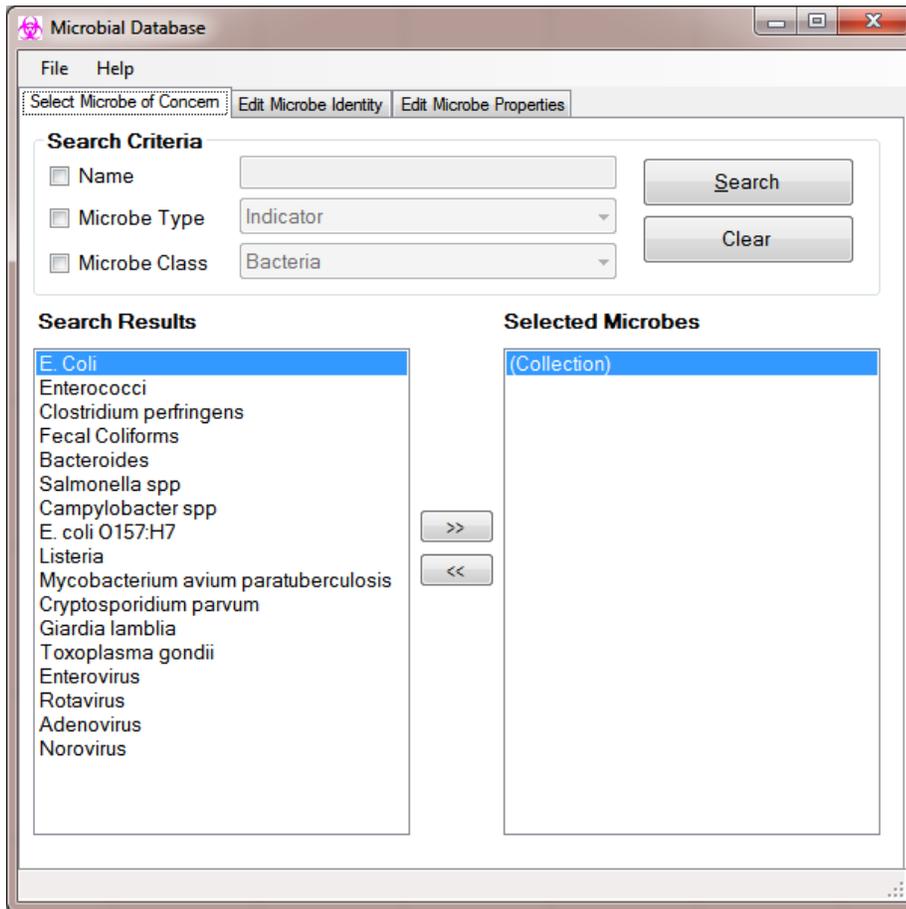
- Execute the MDBE.exe file and the following screen appears. Choose File, then Open.



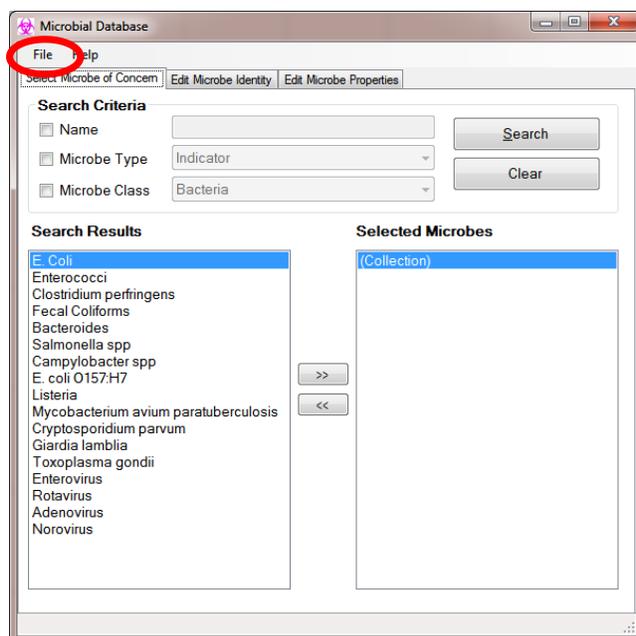
4. Search for Microbes\_Test.mdb in the same folder (shown below) and Open the file.



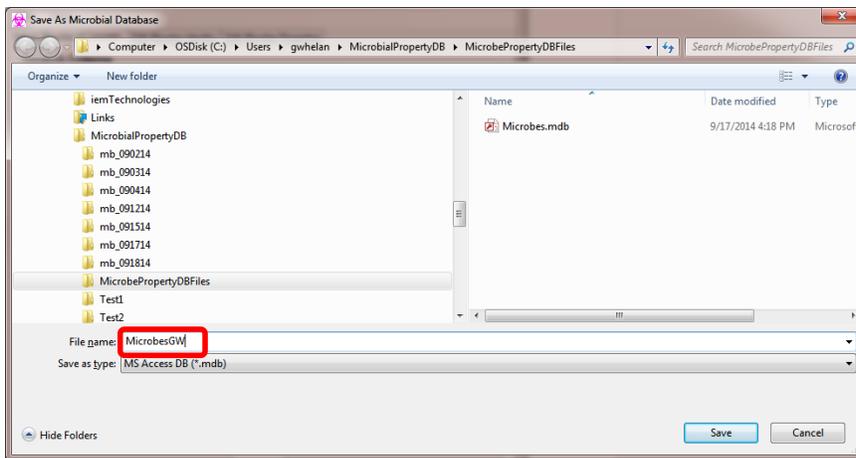
5. The following screen appears:



6. Choosing File,



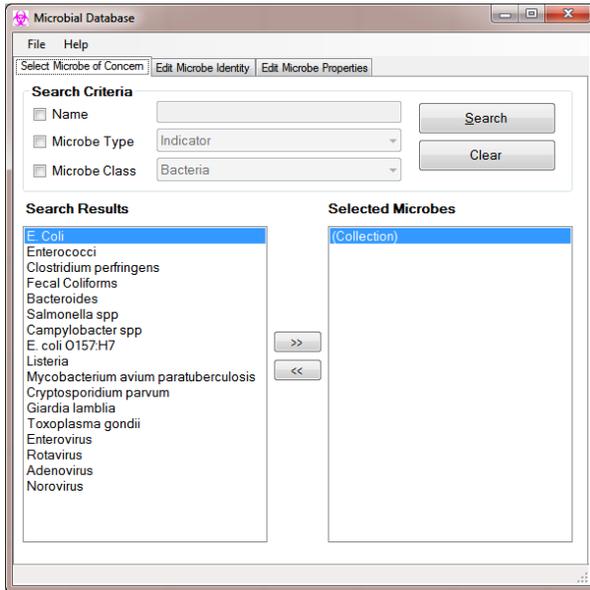
7. The following choices are available:
  - a. New: Creates a new, empty database (no values or references) except the microbe list is retained.
  - b. Open: Opens an existing database.
  - c. Save: Saves the existing changes under the current file name.
  - d. Save As: Saves the existing changes under a new, user-defined file name.
  - e. Save and Exit: Saves the existing changes under the current file name and exits.
  - f. Exit: Exits without saving.
  
8. By choosing New, Open, or Save As, the following screen appears, prompting the user to type the file name. Select File and Save As, and in the File Name text box, type a new file name such as MicrobeGW. Push Save.



## SORT, IDENTIFY, AND SELECT A LIST OF MICROBES

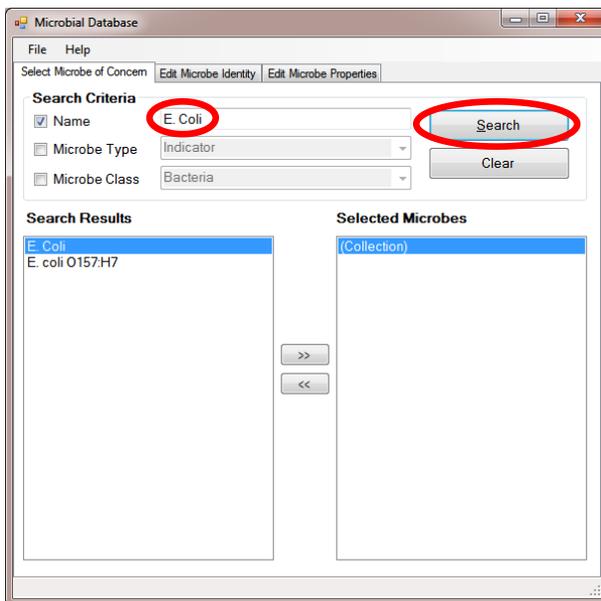
This section describes how a user sorts, identifies, and selects a list of microbes in the database by microbe name, type (indicator or pathogen), and/or class (bacteria, protozoa, or virus).

1. Go to the Select Microbe of Concern tab

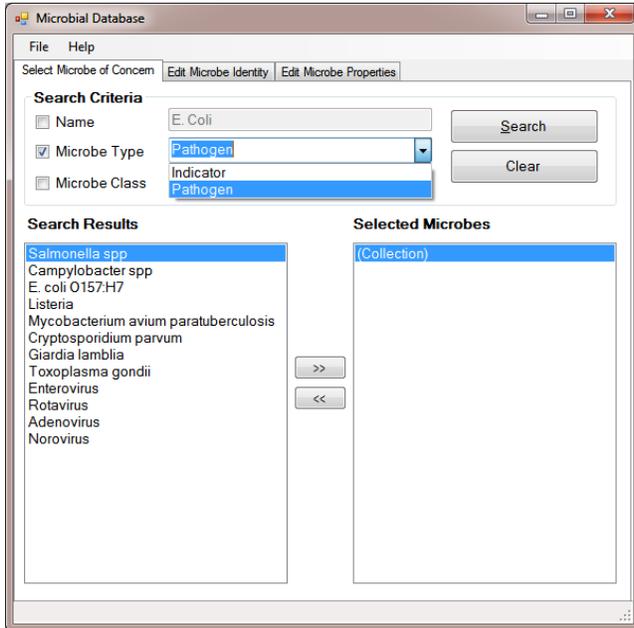


2. There are several ways to search for a microbe:

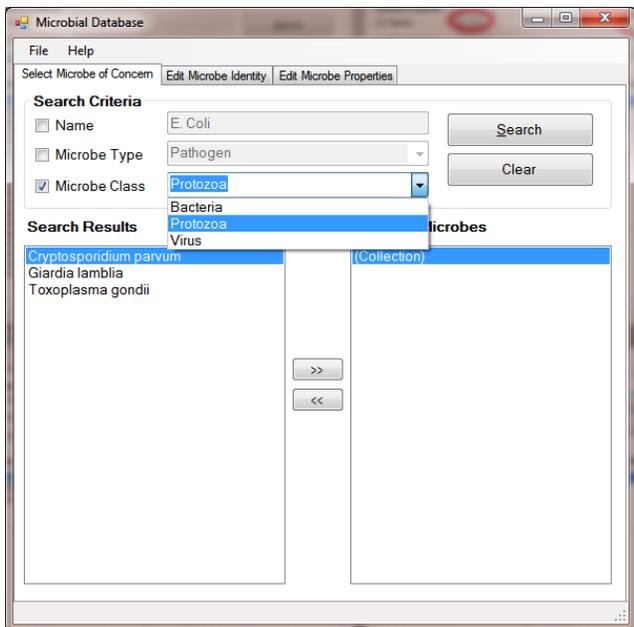
- a. Search by Name: Check the Name box and type "E. coli". Make sure the period and space are included. Press Search to search for all microbes containing the name "E. coli." Results of the search appear under Search Results as seen in the screen capture below.



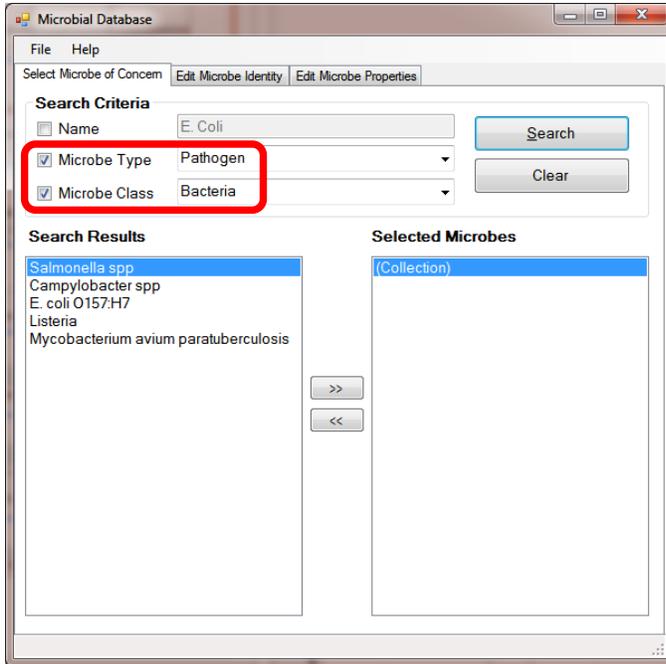
- b. Search by Microbe Type: Uncheck Name box, check the Microbe Type box, choose the down arrow, and select Indicator or Pathogen. Pathogen was chosen in the screen capture below. Pressing Select will search for all microbes classified as Pathogen, providing results under Search Results as noted below.



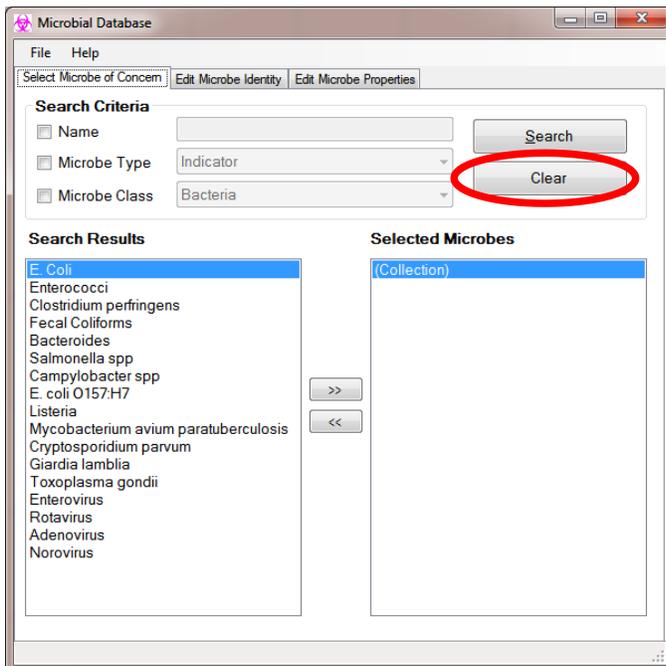
- c. Search by Microbe Class: Check the Microbe Class box, choose the down arrow, and select Bacteria, Protozoa, or Virus; Protozoa was chosen in the screen capture below. Pressing Select will search for all microbes classified as Protozoa, providing results under Search Results, as noted below.



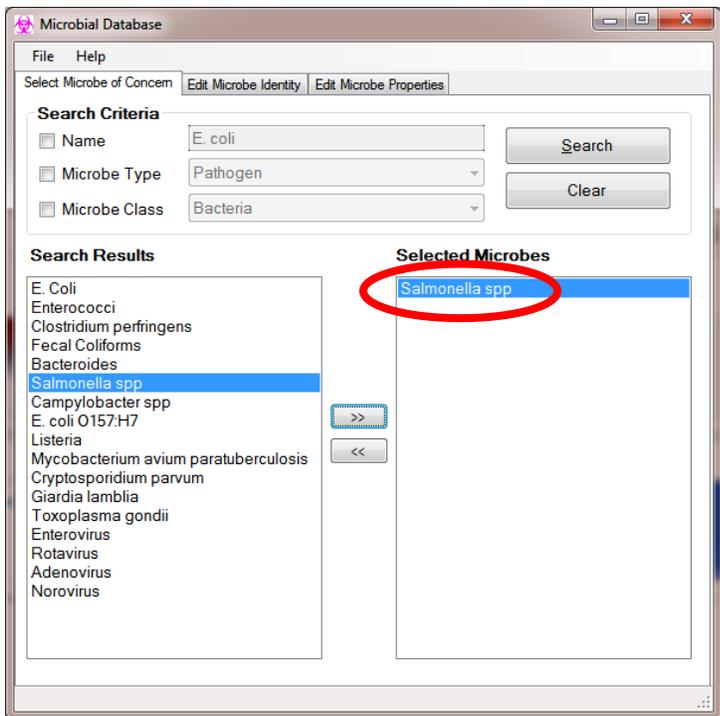
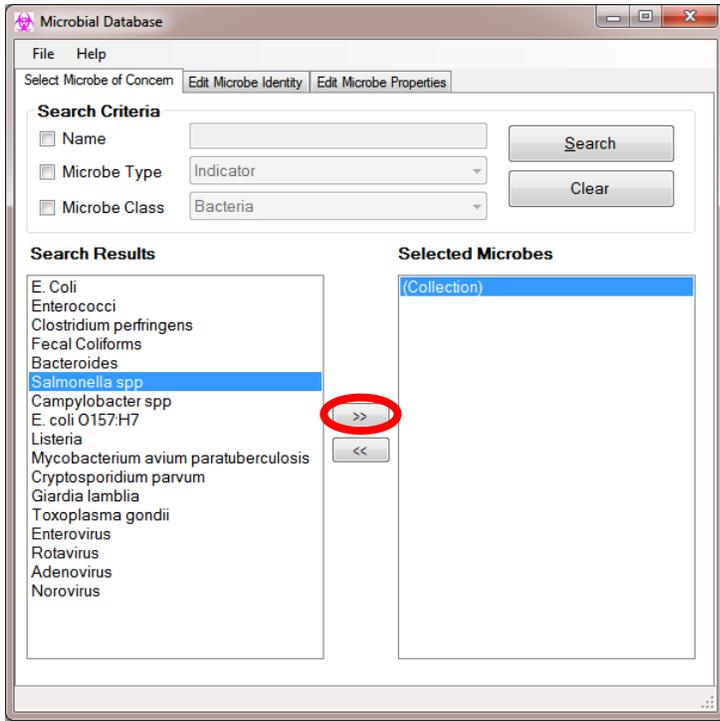
- d. Search by a Combination of Criteria: Check the Microbe Type and Microbe Class boxes, then choose Pathogen and Bacteria, respectively. Pressing Select will search for all microbes classified as Pathogen and Bacteria, providing results under Search Results as noted in the screen capture below.



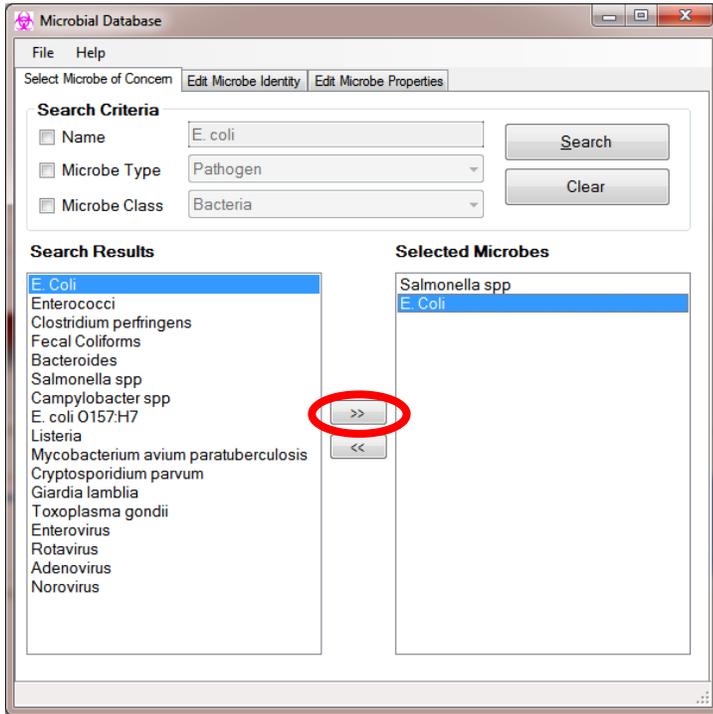
3. To Clear Search Criteria, click Clear and the full list of microbes reappears under Search Results.



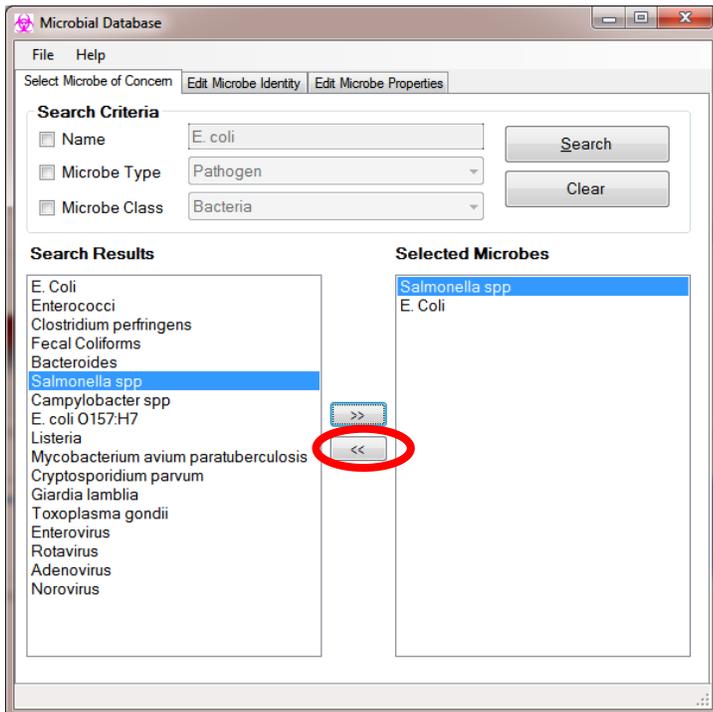
- To select microbes for interrogation or to edit their properties, left-click on the name under Search Results (the name will be highlighted), then left-click on the >> box to move the microbial name to Selected Microbes (see selection of Salmonella spp in the screen capture below).

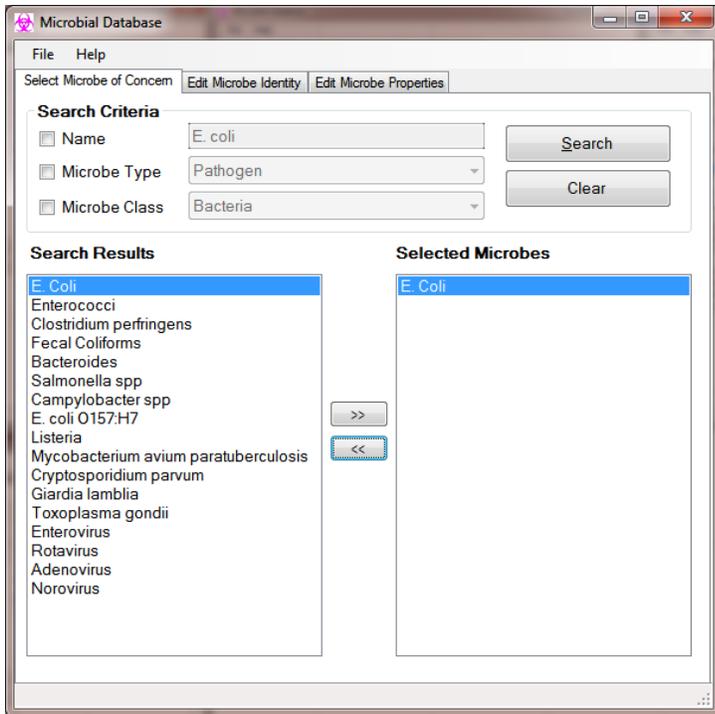


5. Multiple microbes can be chosen and moved from Search Results to Selected Microbes, as illustrated in the screen capture below where *E. coli* has been selected.

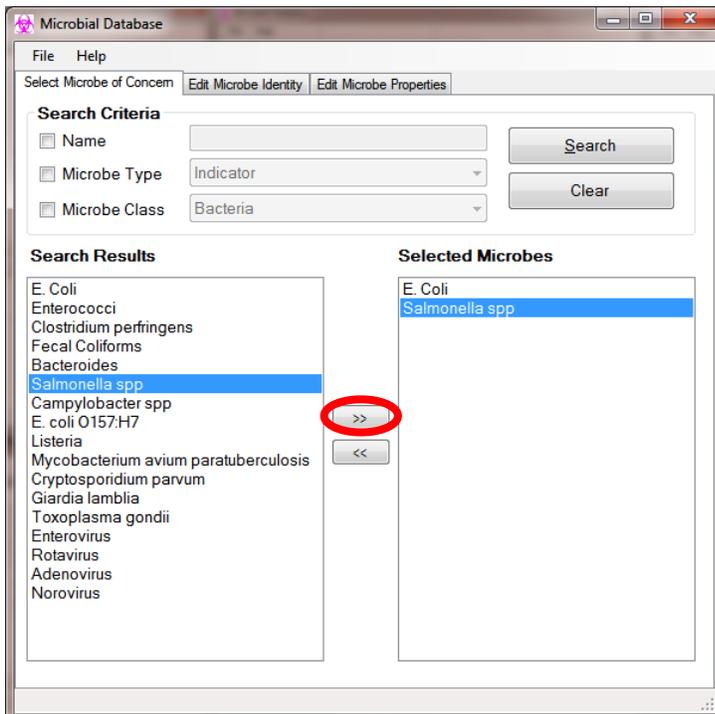


6. To de-select a choice, highlight the microbe in Selected Microbes, and click the << button, as illustrated in the screen capture below where Salmonella spp has been removed.





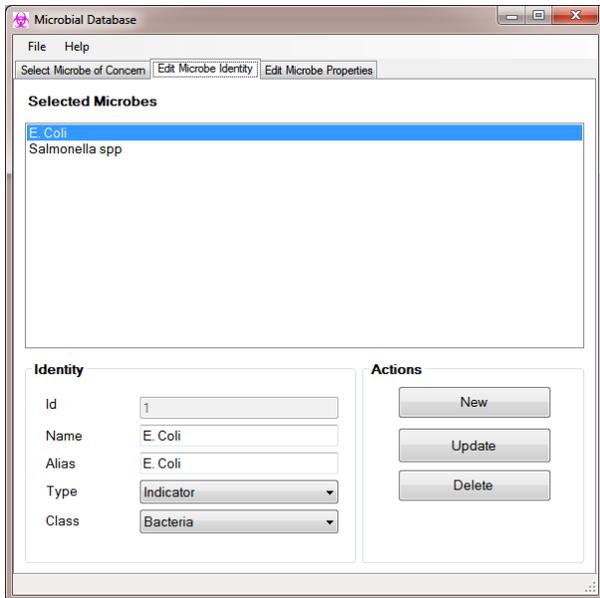
7. Select Salmonella again and move it to Selected Microbes.



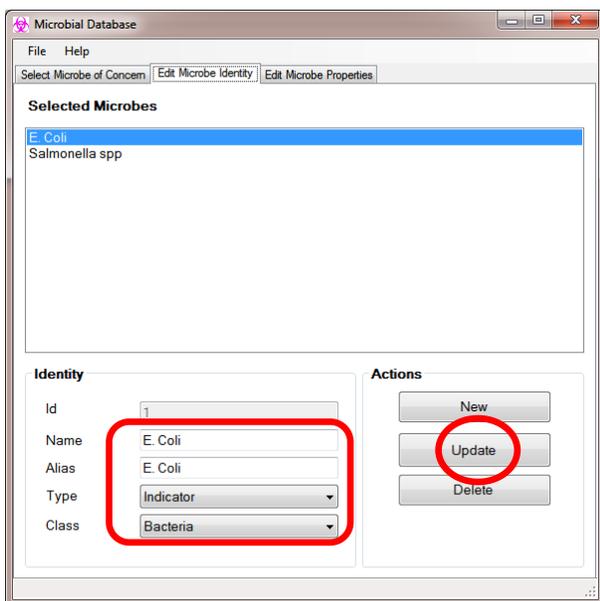
## EDIT IDENTIFICATION CHARACTERISTICS OF EXISTING MICROBES, OR CREATE IDENTIFICATION CHARACTERISTICS OF A NEW MICROBE

This section describes how a user edits identification characteristics of existing microbes or creates identification characteristics of a new microbe.

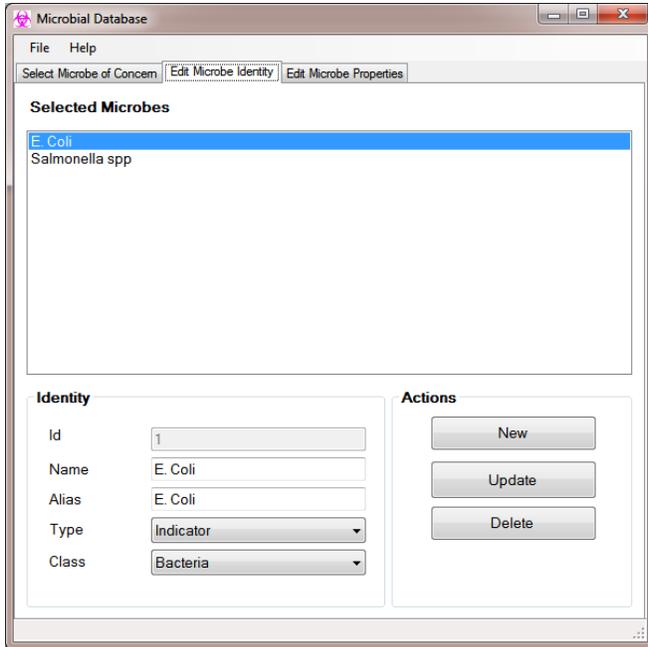
1. To edit identification characteristics of existing microbes or create them for a new microbe, left-click on the Edit Microbe Identity tab.



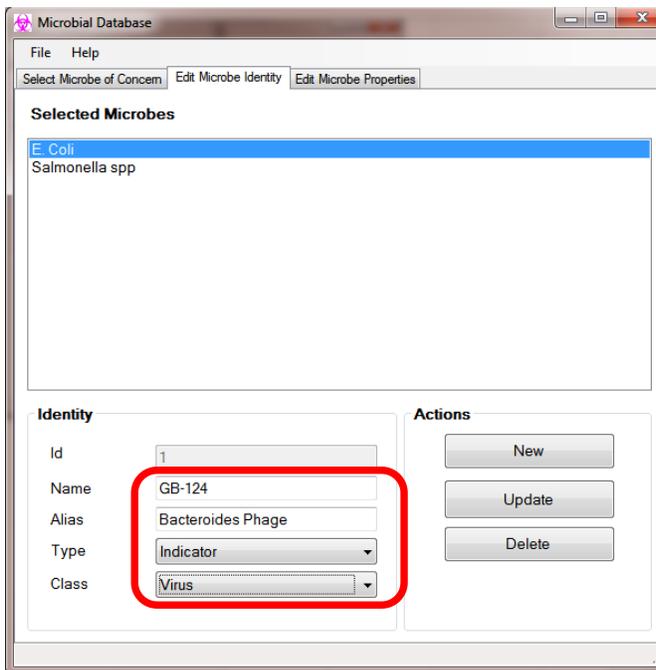
2. To change information in the Identity section (Name, Alias, Type, and/or Class), edit the information and choose Update. This will not change the "Id," but will change information associated with it.



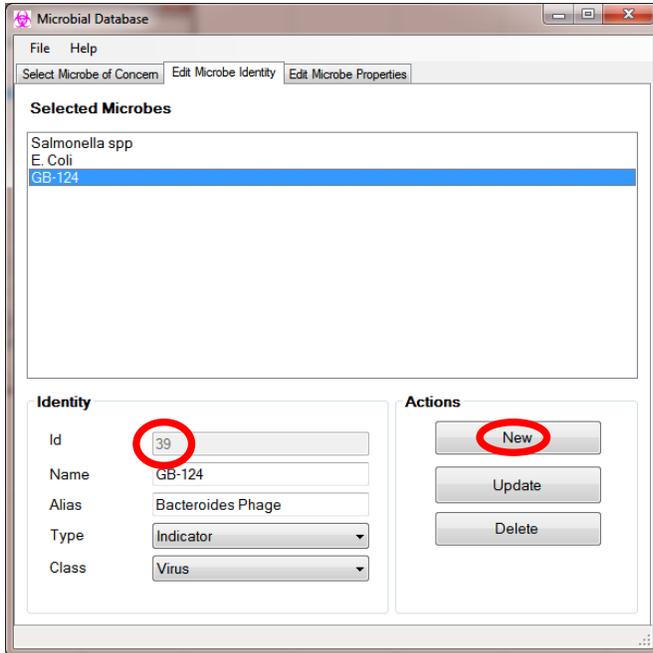
- One way to create and register a new microbe is to select an existing microbe, rename and save it; the original microbe remains unchanged. To demonstrate, highlight E. coli in Selected Microbes.



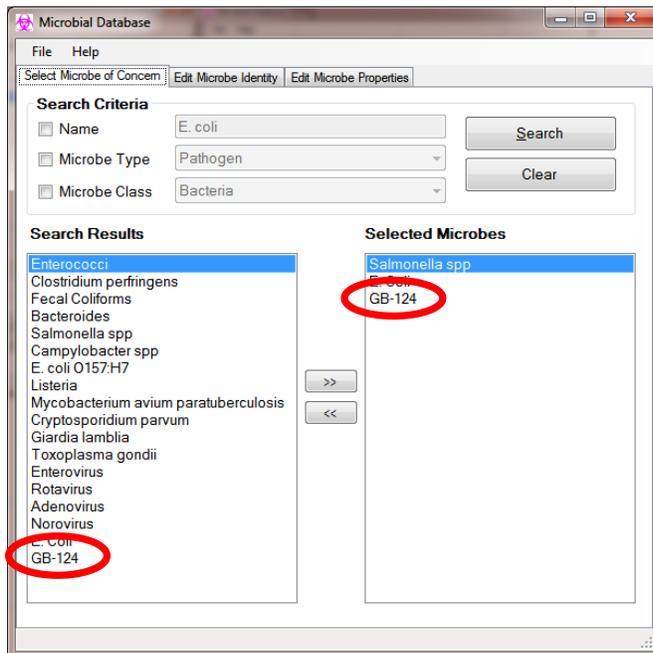
- Register the GB-124 Bacteroides Phage as an indicator virus. Edit the Identity by changing the Name to GB-124 and the Alias to Bacteroides Phage. Under Type, click the down arrow and choose Indicator. Under Class, click the down arrow and choose Virus.



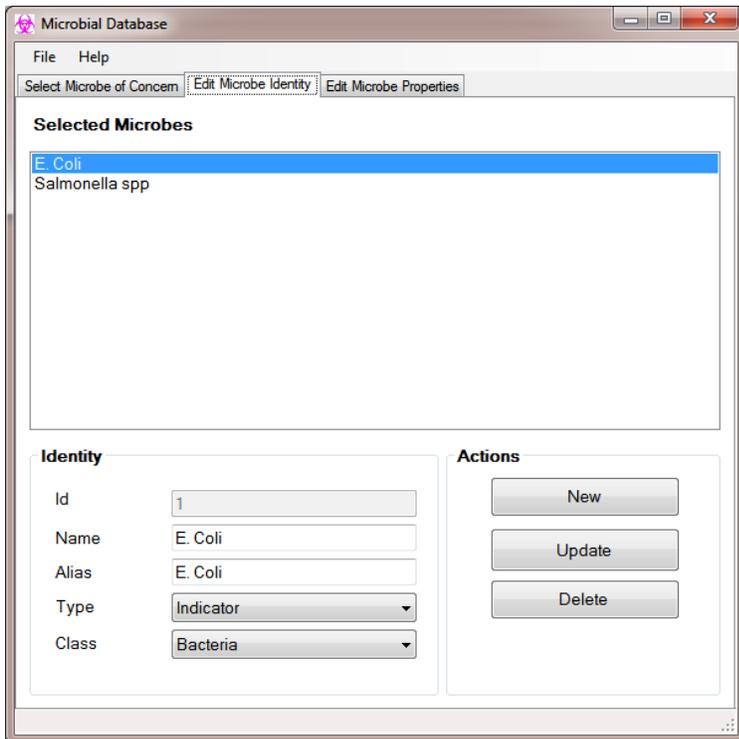
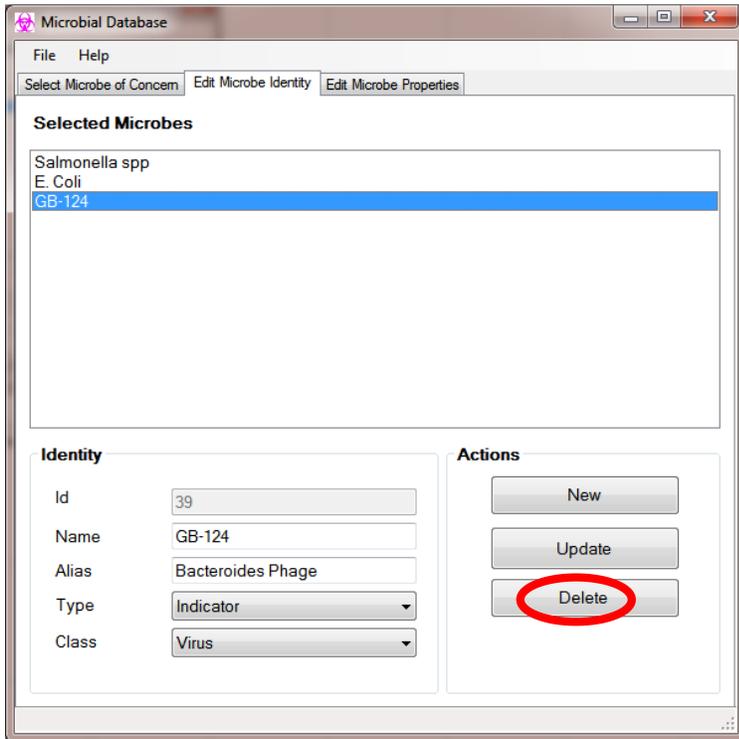
- Under Actions, click New and select GB-124 in Selected Microbes. This will register the new microbe, assign a new identification (Id) number (i.e., 39), and add the name to Selected Microbes. Select new microbe GB-124 in Selected Microbes, and its information appears under Identity.



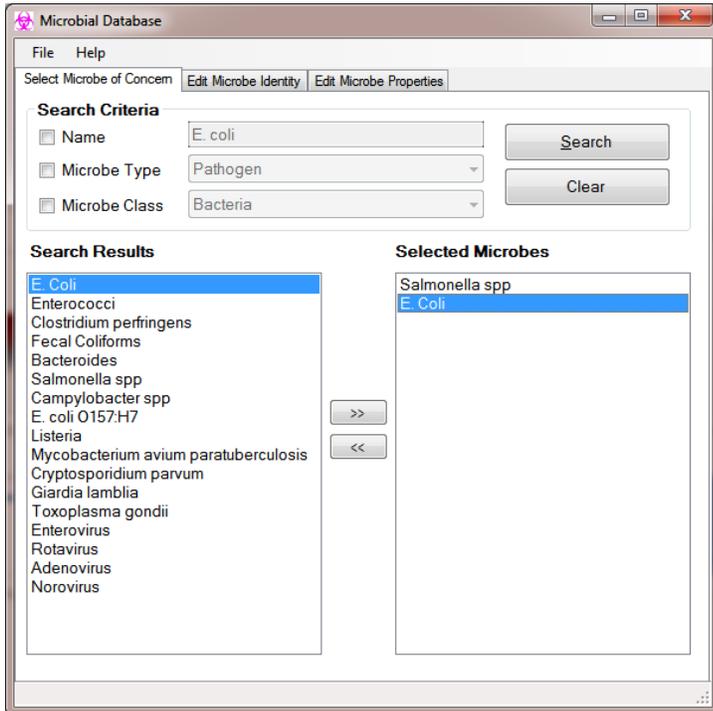
- To verify that the new microbe has been added to the Search list, return to the Select Microbe of Concern tab, and GB-124 will appear in Search Results and Selected Microbes.



- To delete a microbe, go to the Edit Microbe Identify tab, choose the microbe in Selected Microbes, and click Delete under Actions, as illustrated with GB-124 in the screen capture below.



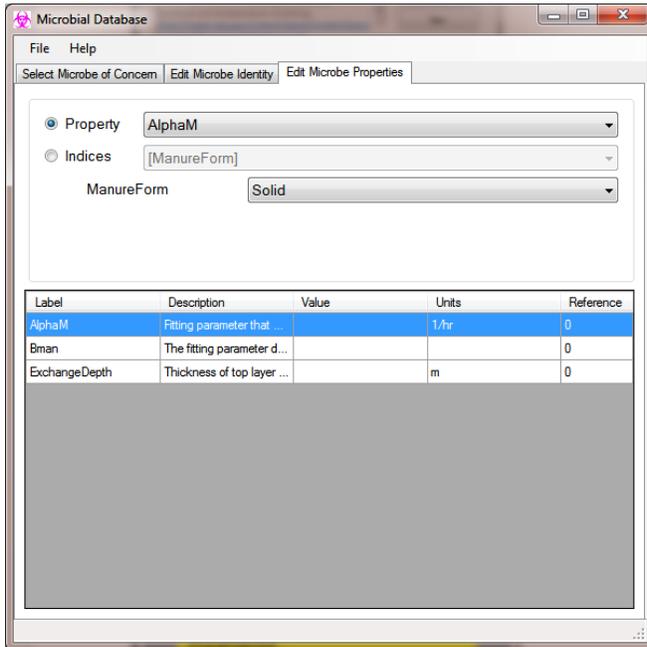
8. To verify that the new microbe has been removed from the Search list, return to the Select Microbe of Concern tab, and GB-124 should be gone.



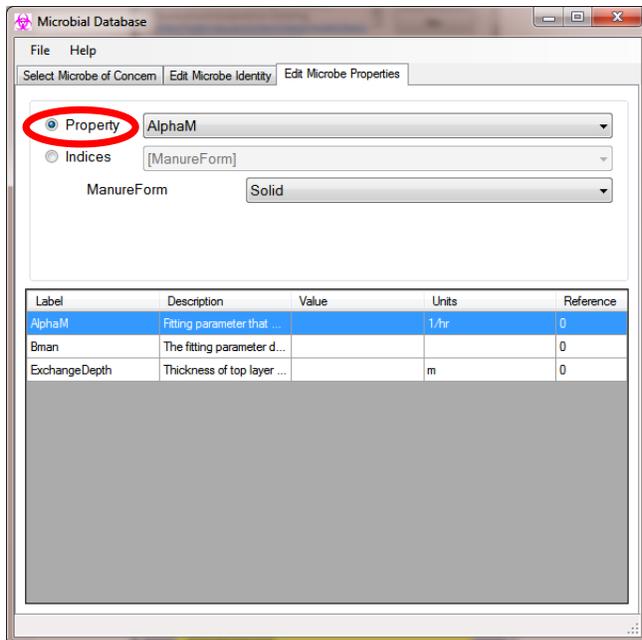
## EDIT MICROBIAL PROPERTIES

This section describes how a user edits microbial properties.

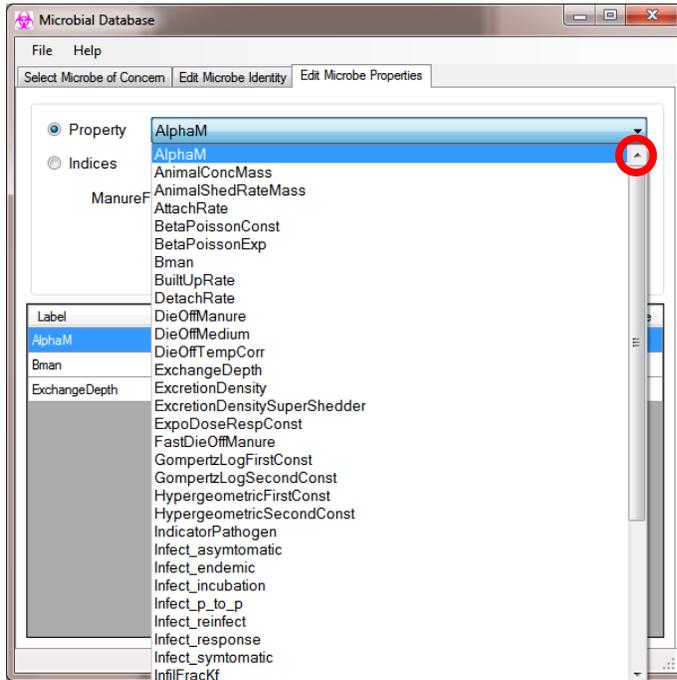
1. To view a list of parameters registered with the database and to edit or assign values and references to them, click on the Edit Microbe Properties tab, and the following screen appears.



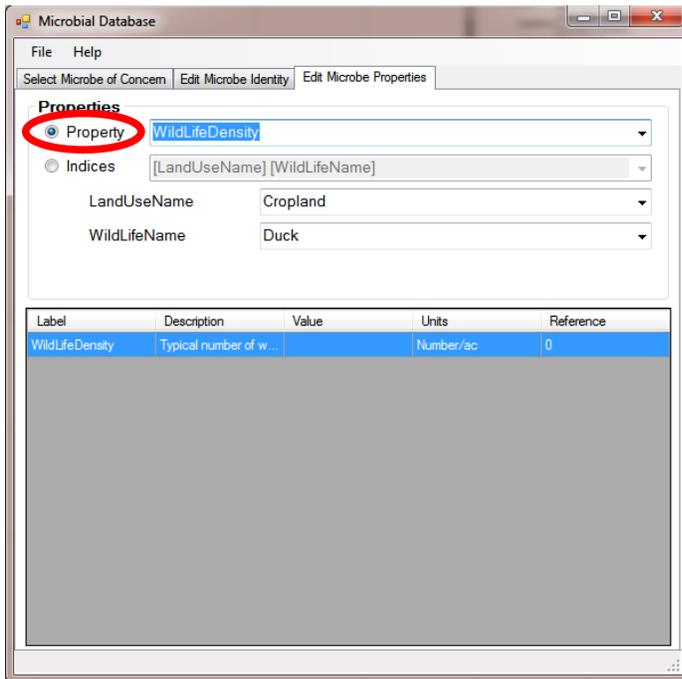
2. Click Property under Edit Microbe Properties, and choose the down arrow beside the Property text box.



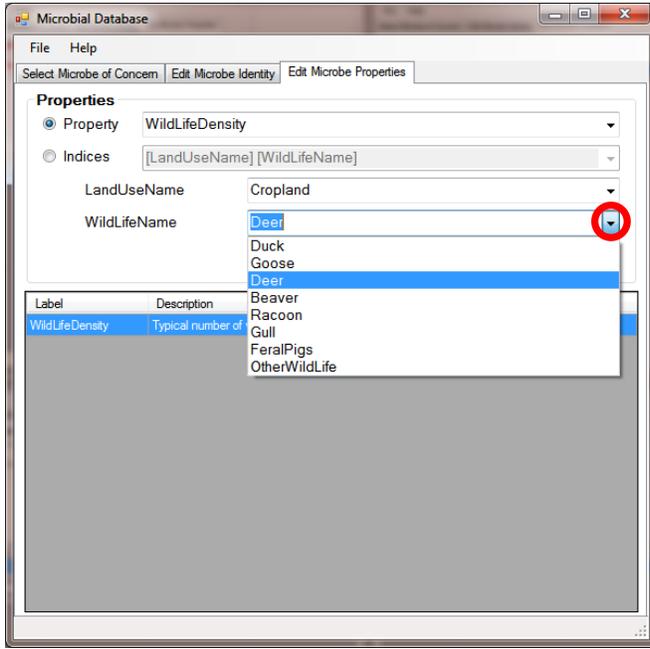
3. A list of parameters registered in the database will appear in alphabetical order.



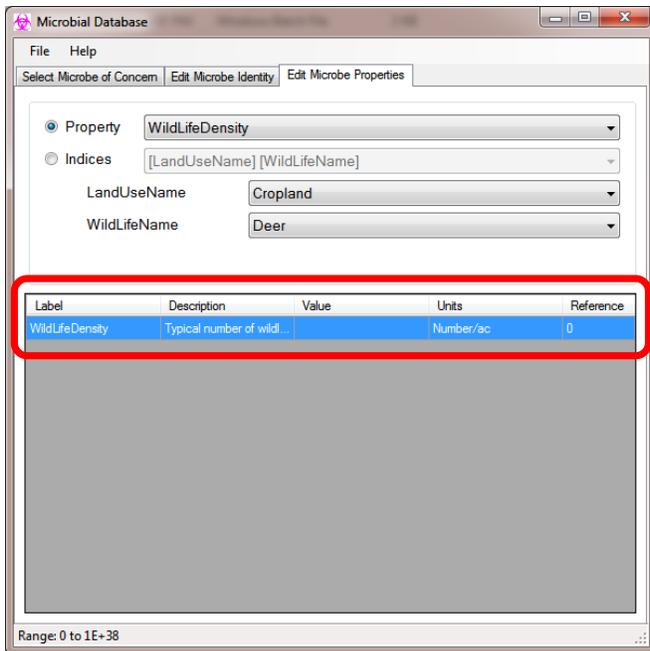
4. This list is consistent with information in Tables 1, 2 and 3. By choosing a parameter such as WildLifeDensity, indices (LandUseName and WildlifeName) and their corresponding choices (Cropland and Duck, respectively) are identified. Additional metadata are provided in the lower-most box, including Name (Label), Description, Value, Units and Reference.



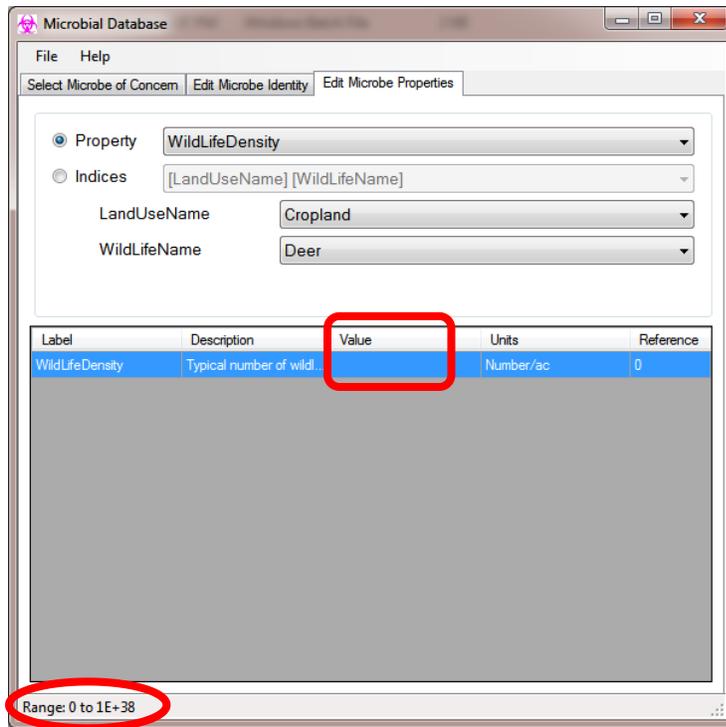
- The user can choose an index under Indices. In this example, LandUseName and WildlifeName are indices for WildLifeDensity (i.e., WildLifeDensity is a function of the two parameters). The user can view choices under Indices, by using down arrow beside the listed indices. In the example below, WildLifeDensity indices chosen are Cropland for LandUseName, and Deer for WildlifeName.



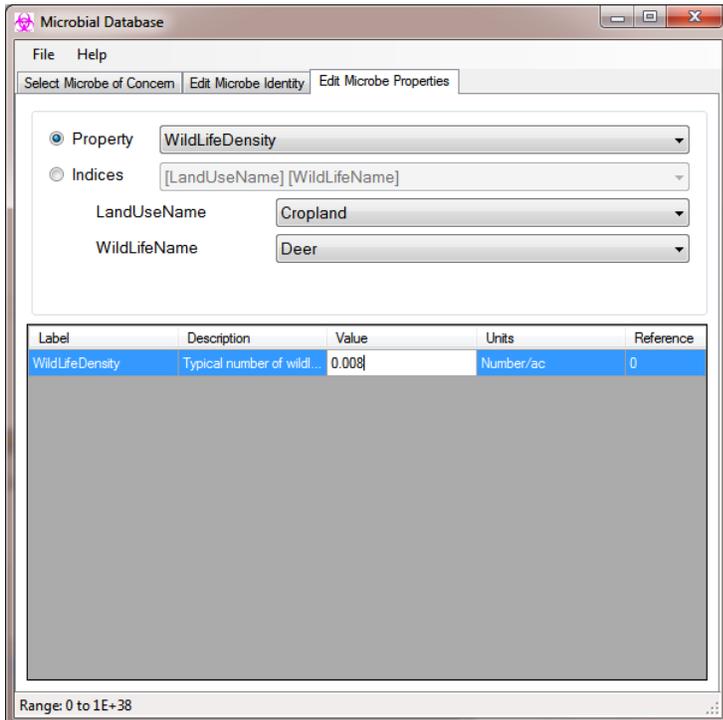
- By choosing the parameter and its indices, the user can view or edit the values and references associated with these choices, as illustrated below where value and reference have yet to be defined.



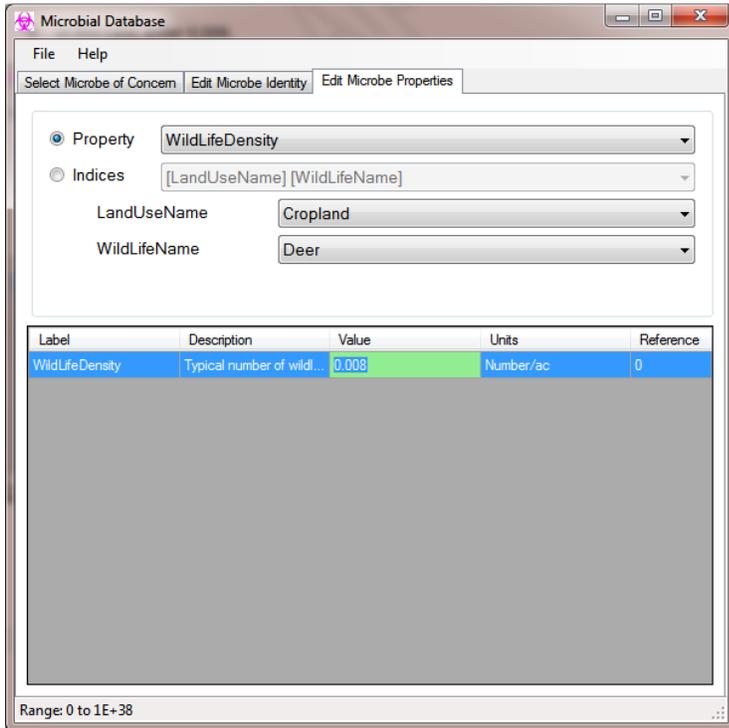
7. To add or edit a value, the user left-clicks on the Value text box and enters the number. Note that the allowable range (minimum and maximum) is provided in the lower left corner.



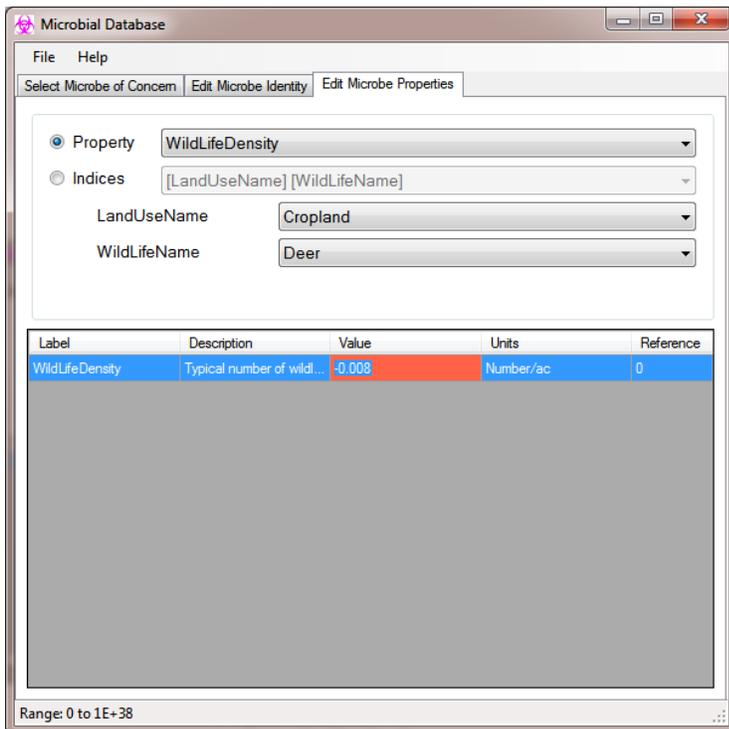
8. Here, enter 0.008.



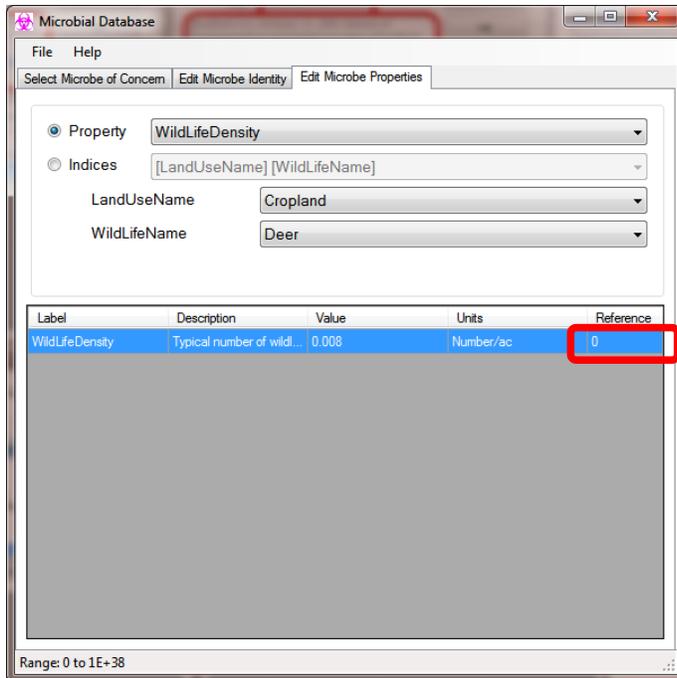
9. If the value is within the range, the box will turn green when it is reselected.



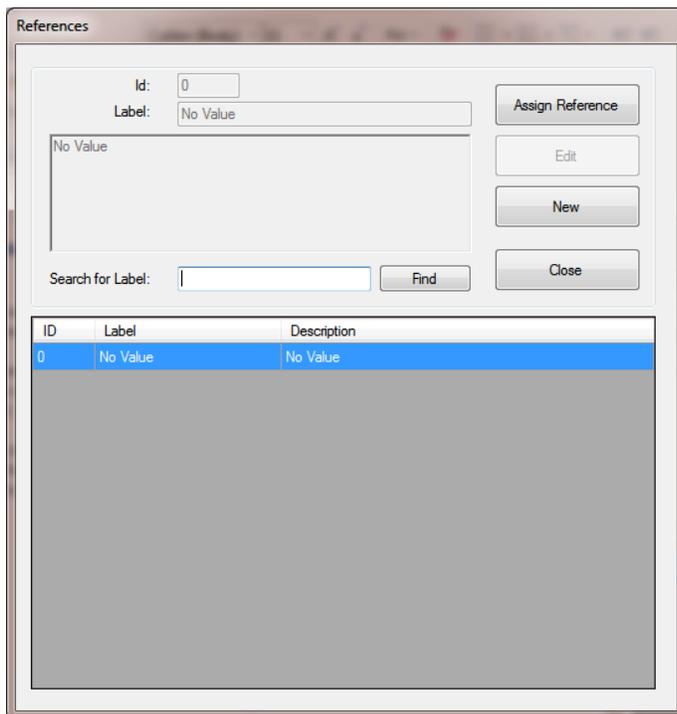
10. If the value is out of range (e.g., -0.008), the box will turn red when it is reselected.



11. Adding references can be executed in a manner very similar to adding values to parameters. Double-click on the Reference box.



12. The following screen appears. The Edit button is grayed out since there is no reference to edit.



13. The Reference screen is designed for two functions, so one must be careful not to confuse them:
  - a. Add the reference to the database reference list. This functionality allows the user to add all references to the database reference list at one sitting versus having to add and assign a reference to a value each time.
  - b. Assign the reference to the value of the parameter. Once the reference is registered, it can easily be assigned to the value of a parameter.

14. In this example, we will add three references to the reference list:

EPA (U.S. Environmental Protection Agency), 2013b. BASINS/HSPF Training, Exercise 10 – Bacterial and temperature modeling. <http://water.epa.gov/scitech/datait/models/basins/upload/Exercise-10-Bacteria-and-Temperature.pdf> (last accessed 23.02.14.).

EPA (U.S. Environmental Protection Agency), 2013c. BASINS user information and guidance, BASINS tutorials and training. <http://water.epa.gov/scitech/datait/models/basins/userinfo.cfm#tutorials> (last accessed 23.02.14.).

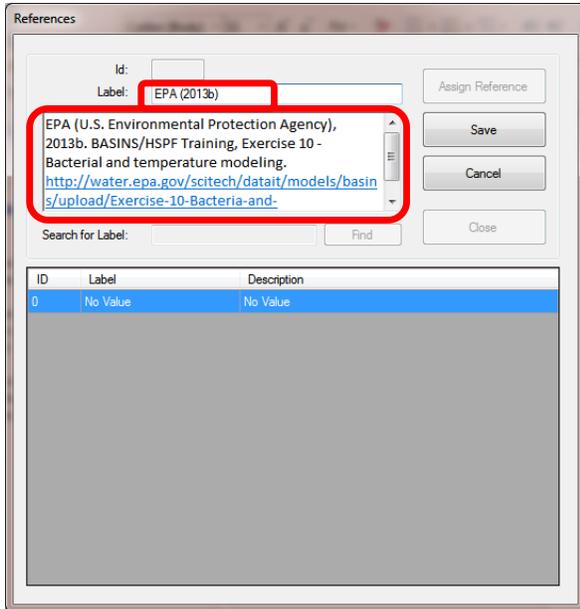
Bradford, S.A., Schijven, J.F., 2002. Release of Cryptosporidium and Giardia from dairy calf manure: Impact of solution salinity. *Environ. Sci. Technol.* 36(18), 3916-3923. DOI: 10.1021/es025573l.

15. To add the first reference, click New.

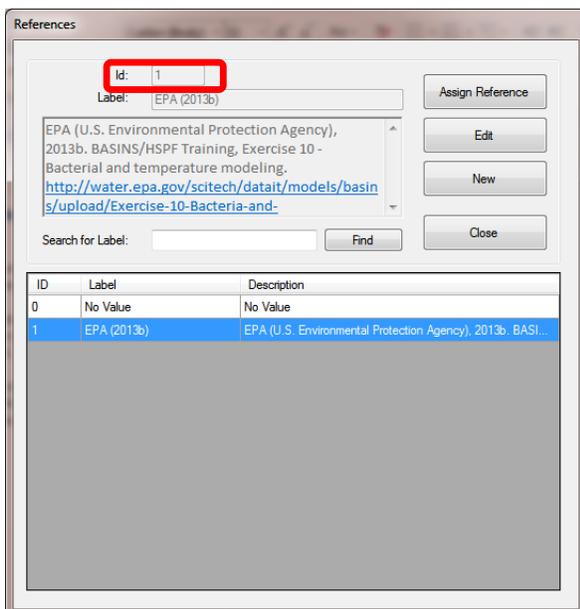
The screenshot shows a software window titled "References". At the top, there are input fields for "Id" (containing "0") and "Label" (containing "No Value"). To the right of these fields are buttons for "Assign Reference", "Edit", "New", and "Close". The "New" button is highlighted with a red circle. Below the input fields is a search area with a "Search for Label:" field and a "Find" button. At the bottom of the window is a table with the following data:

ID	Label	Description
0	No Value	No Value

16. Paste the first reference into the large text box, and add the Label “EPA (2013b)” to its right (under Id). Depending on the operating system, you may need to paste using “Cntl v”. **NOTE: If you have the same Label as one already registered or if the reference is too long, you may receive a “Try again” message.**



17. Click Save to register the reference in the database under “Id:” as 1. The reference is added to the lowest text box. By clicking on the reference (highlighted in blue), the Id, label, and reference appear in upper text boxes. Since this is the first reference, it is assigned “1.” By hovering over the reference description, the reference will also appear as a note. **NOTE: Once a reference is added to the database using Save, the addition is permanent to the database, even if you Exit the database editor without using Save; no parameter value will be saved, however.**



18. To add the second reference, click New and repeat the process. A unique ID (i.e., 2) is assigned.

References

Id: 2

Label: EPA (2013c)

EPA (U.S. Environmental Protection Agency), 2013c. BASINS user information and guidance, BASINS tutorials and training. <http://water.epa.gov/scitech/datait/models/basins/userinfo.cfm#tutorials> (last accessed 23.02.14.).

Search for Label: Find

Assign Reference Edit New Close

ID	Label	Description
0	No Value	No Value
1	EPA (2013b)	EPA (U.S. Environmental Protection Agency), 2013b. BASI...
2	EPA (2013c)	EPA (U.S. Environmental Protection Agency), 2013c. BASI...

19. To add the third reference, click New and repeat the process. A unique ID (i.e., 3) is assigned.

References

Id: 3

Label: Bradford and Schijven (2002)

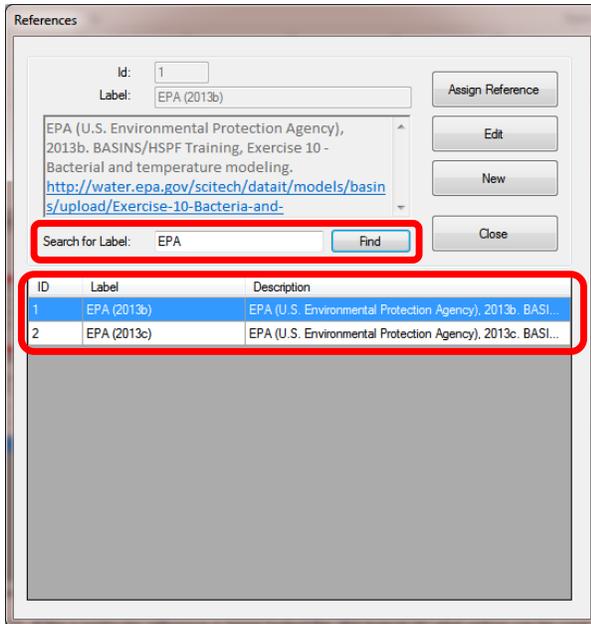
Bradford, S.A., Schijven, J.F., 2002. Release of Cryptosporidium and Giardia from dairy calf manure: Impact of solution salinity. Environ. Sci. Technol. 36 (18), 3916-3923. DOI: 10.1021/es025573l.

Search for Label: Find

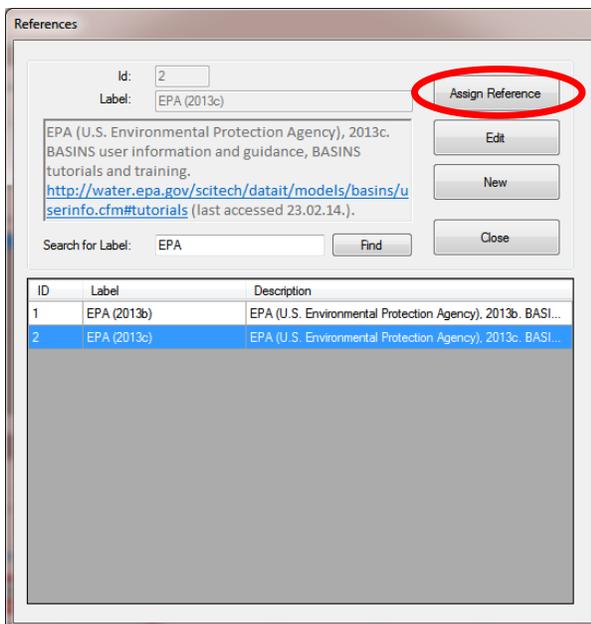
Assign Reference Edit New Close

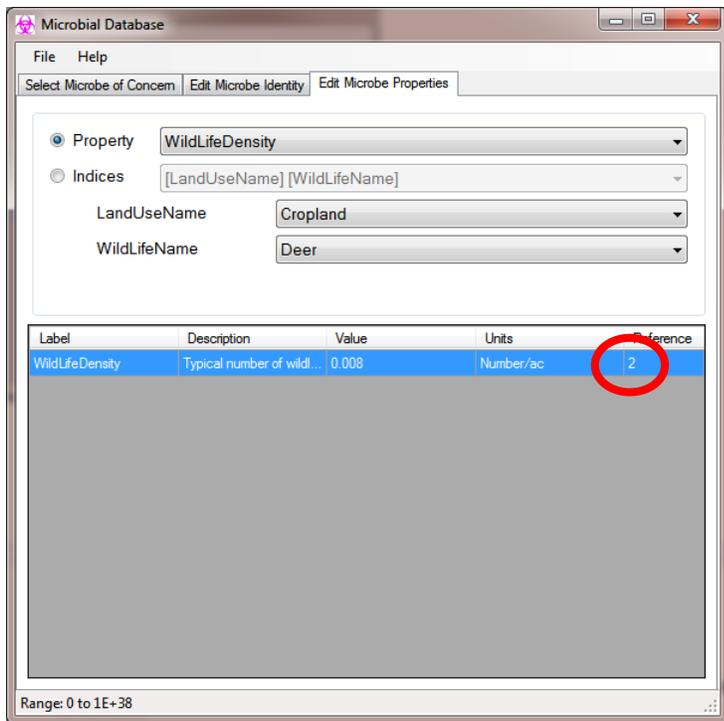
ID	Label	Description
0	No Value	No Value
1	EPA (2013b)	EPA (U.S. Environmental Protection Agency), 2013b. BASI...
2	EPA (2013c)	EPA (U.S. Environmental Protection Agency), 2013c. BASI...
3	Bradford and Schijven (2002)	Bradford, S.A., Schijven, J.F., 2002. Release of Cryptospori...

20. To search for a particular reference, use Search for Label where all references that match the “Search for a Label” entry will be listed. To search all reference labels containing “EPA,” type “EPA” and Find, as illustrated by the screen capture below.

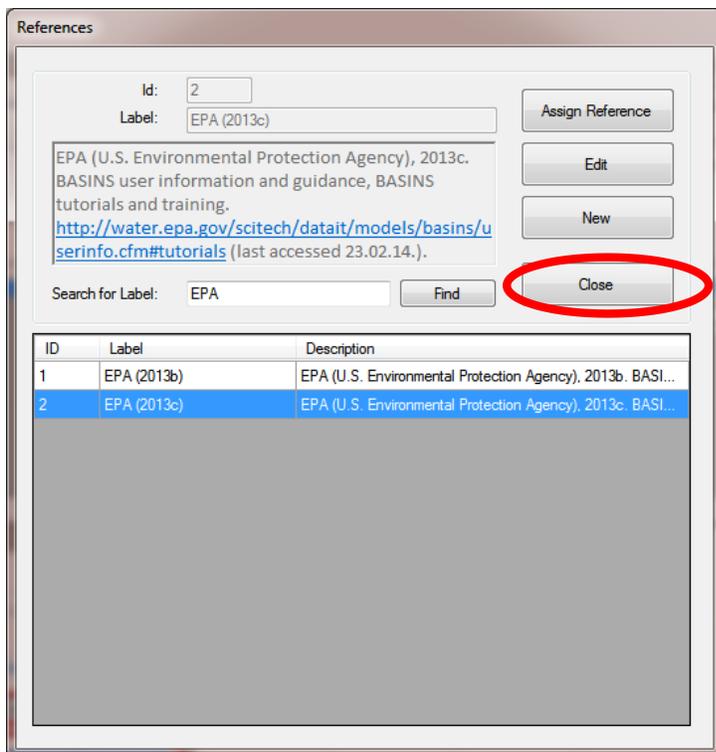


21. To capture the correct reference and assign it to the value in the database, the reference **MUST** be highlighted [see example below for EPA (2013c)], since only the highlighted reference is assigned. **NOTE: When adding references to the database reference list, only one reference can be assigned to each parameter’s value.** After highlighting the EPA (2013c) reference, choose Assign Reference to assign the value. Users then return to the previous screen (Edit Microbe Properties) where the reference ID is automatically assigned to the value.

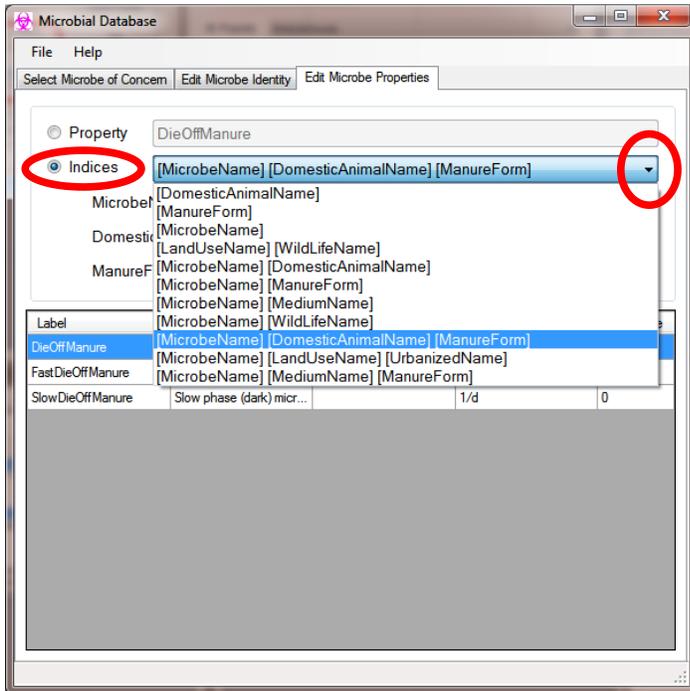




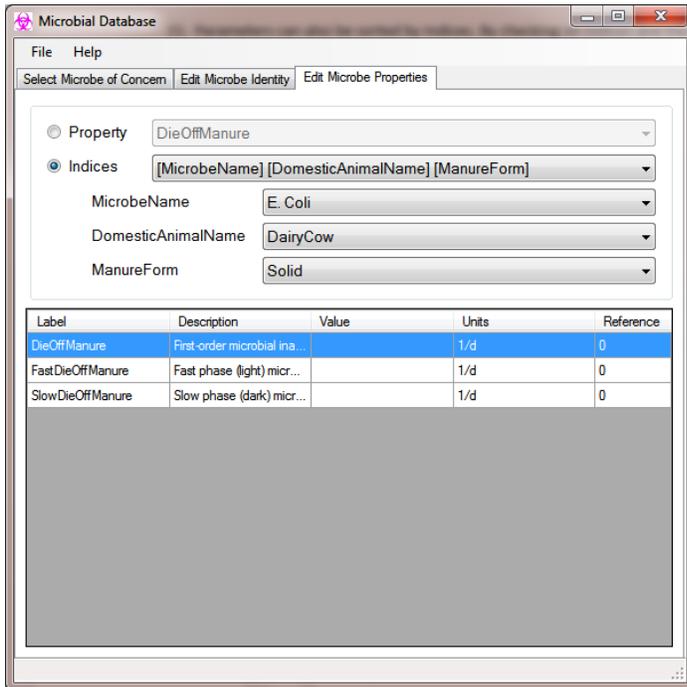
22. If Close is chosen instead, no new reference will be assigned to the value. Upon returning to the previous screen (Edit Microbe Properties), the reference ID will not have changed.



23. Parameters can also be sorted by Indices. By checking Indices and the down arrow, the user can sort parameters by one or more indices associated with the database. For example, choose [MicrobeName][DomesticAnimalName][ManureForm].



24. Three parameters are listed as functions of the three indices. Values and references can be added or edited similarly to previous instructions.



## DISCLAIMER

This document has been reviewed in accordance with U.S. Environmental Protection Agency policy and approved for publication.

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